

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 101491

TO: Sheela Huff

Location: CM1/8B07&8E12

Art Unit: 1642

Friday, August 29, 2003

Case Serial Number: 09/970969

From: Susan Hanley

Location: Biotech-Chem Library

CM1 6B05

Phone: 305-4053

susan.hanley@uspto.gov

Search Notes	
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STIC-Biotech/ChemLib

From: Sent:

Huff, Sheela Friday, August 22, 2003 5:52 AM STIC-Biotech/ChemLib

To: Subject:

RE: search request for 09/970969

1.UG 22 201

Not sure what you mean by only 3 sequences. The RSL (which has been marked "entered") in the file says that there are 6 sequences. The paper copy supplied by applicant also says that there are 6 sequences.

Sheela

-----Original Message-----

From:

STIC-Biotech/ChemLib

Sent:

Wednesday, August 20, 2003 6:30 AM

To:

Huff, Sheela

Subject:

RE: search request for 09/970969

----Original Message-----

From: Huff, Sheela

Sent:

Tuesday, August 19, 2003 6:12 AM

STIC-Biotech/ChemLib To:

Subject: search request for 09/970969

THERE ARE ONLY 3 SEQ FOR THIS NUMBER. **MAUDE**

Please search and interference search SEQ ID No. 1-6 of the above application.

Thanks--

Sheela Huff Art Unit 1642 CMA-8807 mailbox 8E12 305-7866

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

/ENDOR/COST (where appl	ic.)
STN:	
DIALOG:	
Questel/Orbit:	
DRLink:	
Lexis/Nexis:	
Sequence Sys.:	
WWW/Internet:	
Other (specify):	

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Scoring table:

Searched:

Database

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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result ş Novel modified annexin useful for imaging vascular thrombi and

Annexin V/urokinas Vascular anti-coag Plasmid contg. pla Human cDNA #162 di Endonexin II compl

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AAC91369 AAC91368 AAC91370 AAA11241 AAN91353

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ABX63162 AAN91821

Description

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                                                                  ACCTCTCTTTATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTG
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transplant rejection; ds.
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Matches 979; Conservative
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P-PSDB; AAB50863.
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                                                                                                     The present sequence encodes a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response tro a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radiouncide and retain annexin bloactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.
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  apoptosis, has N-terminal chelation site comprising amino acid
extension which comprises a glycine and a cysteine residue
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100.0%; Score 981; DB 22; Length 981;
Best Local Similarity 100.0%; Pred. No. 4.5e-275;
Matches 981; Conservative 0; Mismatches 0; Indels 0
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                                                                  Claim 26; Page 31-33; 39pp; English
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Modified human annexin nucleotide sequence, SEQ ID

(first entry)

16-MAR-2001

AAC91370;

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BP 981

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin bloactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.
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Pred. No. 1.1e-273;
0; Mismatches 3; Indels 0;
                                                                             Human; annexin; chelation site; nuclear imaging; apoptosis;
transplant rejection; ds.
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  or 3' ends of the sequence"
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                                                                                                                                                                                                                                                                                                                                             Annexin V, which has high affinity for active thrombocytes, is used as a carrier molecule to build a thrombous-targeting thrombolytic fusion protein. The protein is the result of expression of a fusion gene (this sequence) comprising the Annexin V gene and a low-molecular urcklanses gene, in insect cells. The Annexin V scu-PA-32 fusion protein expressed in insect cells train The Annexin V scu-PA-32 fusion protein, expressed in insect cell strain The Annexin V scu-PA-32 fusion protein, thrombocytes and has the fibrinolytic activity of uroklasse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 TATGAACTGAAACATGCCTTGAAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.7%; Score 958.6; DB 21; Length 1803; 98.6%; Pred. No. 2e-268; Live 0; Mismatches 14; Indels 0;
                                                                                                                                                                                                                        New thrombolytic fusion protein for targetting thrombus fusion of Annexin V and urokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1803 BP; 495 A; 415 C; 462 G; 431 T; 0 other;
                                                 (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD
                                                                                                                                                                                                                                                                                                 Claim 2; Page 2-4; 20pp; Chinese.
99CN-0113524
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les 967; Conservative
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ATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAA
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Pred. No. 2.7e-268;
0; Mismatches 5;
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                                              Sequence 1466 BP; 423 A; 291 C; 327 G;
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ilarity 99.5%;
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ATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTA
              ATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACGCGGGGAGACTTCTGGCAATTTA
                               GAGCAACTACTCCTTGCTGTTGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAG
                                       ACCTCTCTTTATTCCATGATTAAGGGAGATACATCTGGGGGACTATAAGAAAGCTCTTCTG
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P-PSDB; AAP91953.
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                                             GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT
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ental coagulation inhibitor - useful for the prevention thromboses or disseminated intra-vascular coagulation.
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WPI; 1991-329110/45.
P-PSDB; AAP80511.
                                             (KOWA ) KOWA CO LID
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12-NOV-1990
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JP03219875-A.
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23-JUL-1987;
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This invention relates to a combination comprising several CDNAs that are differentially expressed in activated vascular tissue. The invention are differentially expressed in activated vascular tissue. The invention calso discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have been compounded to cardinati, hypotensive, antidiabetic; gynaecological; vasorropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several conflection or compound that specifically binds a cDNA of the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or compounds to identify an antibody to the protein that can combinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia-combinate protein from a sample. The cDNAs are useful for diagnosing pre-patchologic disorders, and chronic combnas are useful for diagnosing pre-patchologic disorders, and chronic combnas are useful for diagnosing pre-patchologic disorders, or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence companions of the protein. The present sequence companions of the protein that is differentially expressed in
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Note: The sequence data for this patent did not form part of the
specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated vascular tissue -
Human cDNA #162 differentially expressed in activated vascular tissue.
                                              Human, gene; ss; vascular tissue; cytostatic; atherosclerosis;
cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;
cerebroprotective; gene therapy; vascular disease; cancer; coronary;
artery disease; hypotrenal, or diabetes; pre-eclampsia; restenosis;
ischaemia-reperfusion injury; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http.seqdata.uspto.gov/sequence.html?DocID=20020137081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page -; 18pp; English.
                                                                                                                                                                                                                                                                                                                                            08-JAN-2002; 2002US-0044090.
                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000US-222469P. 08-JAN-2001; 2001US-260483P.
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562 GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC 502 AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT

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99.8%; Pred. No. 6.3e
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Local Similarity 99.8 tes 958; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence encoding anticoagulant PP4 protein. This inhibits blood coagulation at the thromboplastin stage. The derived protein is 320 amino acids. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Anticoagulant; PP4 protein; thromboplastin.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                              Score 956.8; DB 10; Length 1605;
Pred. No. 6.3e-268;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                             Sequence 1605 BP; 447 A; 337 C; 366 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                          hENII is a calcium and phospholipid binding protein. (Updated on 25-MAR-2003 to correct PA field.)
                  Location/Qualifiers
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Homo saptens (human).
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P-PSDB; AAP91021.
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               461 A; 322 C; 351 G; 441 T; 0 other;
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                              Score 956.4; DB 10
Pred. No. 8.2e-268;
0; Mismatches 6;
(Updated on 25-MAR-2003 to correct PI fleld.)
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               Sequence 1575 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                              PAP-I; anticoagulant; anti-inflammatory agent; phospholipid; phospholipase A2; disseminated intravacular coagulation; human placenta; deep vein thrombosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human proteins having anticoagulant and antiinflammatory activity - isolated from biological fluid by anion-exchange chromatographoc media.
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                                                                                                                                                                                                                                                                                                                                                              anticoagulant production
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Pred. No. 1.8e-267
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                                                                                                                                                                standard; cDNA; 1454
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                                                                                                                                                                                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                          This sequence, or a fragment of it, is used in the construction of DNA sequences encoding hybrid phospholipid-binding proteins (PBP) comprising at least one lipocortin phopholipid binding domain (PBP), or year of PAP-I, joined to a gla-domainless vitamin K-dependent protein, e.g. protein to a gla-domainless vitamin K-dependent A human placenta cDNA library was screened using affinity-purified antibody against PAP-I in order to obtain this cDNA. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                   Recombinant prodn. of hybrid phospholipid-binding proteins comprising lipocortin phospholipid-binding domain and vitamin K-dependent protein
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Matches 957; Conserv
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                           CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA
                                                                                             GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGCCCTCTATTATGCTATGAAG
                                                                                                                                                                                                                                           Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha (Glu22).
                                                                                                                                                                                                                                                            Vascular anticoagulating protein (VAP) VAC-alpha; anticoagulant; antiinflammatory; phospholipase inhibitory.
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87DE-3710364.
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Reutlingsperger
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28-MAR-1987;
28-MAR-1987;
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mat_peptide
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                                                                                          The DNA is produced by determining the amino acid sequence of isolated and highly purified VAPs, constructing DNA probes on the basis of this sequence, using the probes to search through suitable cONA libraries, isolating cDNA that hybridises with the probes, by inserting the cDNA into a suitable vector, and using the vector to transform a host organism. VAC-alpha has anticoagulant activity under certain ordinates, but loses this activity in the event of severe bleeding. It acts by inhibiting conversion of factor x to factor Xa and conversion of prothrombin to thrombin. It is structurally related to lipocortin I (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and has similar antiinflammatory and phospholipase inhibitory activity. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
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                     agents,
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 954.6; DB 9;
Pred: No. 2.6e-267;
0; Mismatches 4;
vascular anti:coagulating proteins - ul as thrombin inhibitors, antiflammatory
                                                            German.
                                                            4/1-4/3; 183pp;
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11 Similarity 99.6%;
957; Conservative
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organism. VAC-alpha has anticoagulant activity under certain conditions, but loses this activity in the event of severe bleeding. It acts by inhibiting conversion of factor X to factor Xa and conversion of prothrombin to thrombin. It is structurally related to lipocortin i (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and thas similar antilifianmentcry and phospholipase inhibitory activity. (Updated on 25-WAR-2003 to correct PR field.)
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                                                                                                                           Length 963;
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                                                                                                   963 BP; 284 A; 183 C; 242 G; 254 T; 0 other;
                                                                                                                       Score 953.6; DB 9;
Pred. No. 4.2e-267;
0; Mismatches 4;
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Best Local Similarity 99.6%;
Matches 956; Conservative
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                                                                                                                                                        1CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGAT
                                                                                                                        AATTCAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGT
                                                                   GGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA
                        TGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGAA
                                                                                                                                                                                                                                                                                                                                                              Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
35..963
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Reutlingsperger
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Adolf G, Re
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                   321
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                   AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC
 GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGAAG
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CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATT
                 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lipocortin-V was isolated from a lambda gtl0 human peripheral blood lymphocyte cDNA library with rat lipocortin-V cDNA of lambda RLipo V-1 as probe. Lipocortins are anti-inflammatory agents and can be used to treat arthritic, allergic, dermatologic, ophthalmic, and collagen diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                            Human lipocortin-V; lambdaRLipo V-1; anti-inflammatory agent.
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complement (143..1102)
/*tag= a
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arthritic, allergic, dermatologic,
                                                                                                                                                                                                                                                                                                                                                                                                    involving inflammatory processes.
                                                                                    ВР
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                                                                                  AAN90599 standard; cDNA; 1574
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Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; antagonists may have neuroprotective; cytostatic; cardioactive; general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The Invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated of polynucleotide sequences may be used for detection of lung cancer. Chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat diagnostic or research pulmonary, cardiovascular, reproductive, gastrointestinal, immune, muscular, renal, and proliferative disorders such as neural, immune, muscular, renal, and proliferative disorders. The proteins may also be used in the treatment of vounds and infectious diseases. Polynucleotide sequences AAF18433 and peptide AAB58549 are used in the course of the invention for the
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                                                                                                                                                                                                                     Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
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Pred. No. 3.9e-264;
0; Mismatches 3;
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                                                                       SCI INC
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Best Local Similarity 99.6%;
Matches 956; Conservative
08-MAR-2000; 2000WO-US05918
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(ROSE/) ROSEN C A.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Modified human ann	Modified human ann	Modified human ann	Vascular anti-coad	Plasmid contq. pla	Human cDNA #162 di	Endonexin II compl	. Anticoagulant PP4
TES			:	_	_					
SUMMARIES		a	AAC91368	AAC91369	AAC91370	AAN91353	AAN81113	ABX63162	AAN91821	AAN90112
		80	22	22	22	10	5	25	10	10
		Query e Match Length DB ID	981	981	981	1466	1567	1578	1605	1575
	æ	Ouery Match	100.0	66.1	99.5	7.76	97.5	97.5	97.5	97.5
		Score	981	977.8	976.2	958.2	956.8	956.8	956.8	926.6
		Result No.	-1	7	e	4	'n	9	7	80

Annexin V/urokinas	PAP-I CDNA from hu	PAP-I. Homo sapie	Sequence encoding	Sequence encoding	Human lipocortin-V	Lung cancer associ	Toxicologically re	Mouse ischaemic co	Rat seguence diffe	Human annexin V pr	Modified annexin p	Human novel polynu	PAP-I-protein C fu	PAP-I-protein C fu	Bovine EST associa	Bovine EST associa	Coding strand of c	Bovine EST associa	cDNA encoding huma	Human cancer assoc	Human cervical can	Human ovarian tumo	Human cDNA #220 di	Human placenta-der	DNA encoding novel	c	₩	cDNA of human plac	z	olon	. Phase-1 Rat CT ger	Human lung cancer-	Human lung cancer	ang	Annexin XI qene in
AAA11241	AAN82107	AAQ12679	AAN80801	AAN80873	AAN90599	AAF18269	ABZ83344	AB199289	ABK63699	AB221925	ABZ21926	ABX05088	AAQ12681	AAQ12680	ABX47939	ABX36749	AAN90772	ABX42696	ABS76372	AAC77826	AAH72826	AAZ77514	ABX63220	AAQ02888	AAS93800	ABK84730	ABN97346	AAQ02887	ABX72249	ABQ59306	ABT09335	AAC65957	ABQ92362	ABL49176	AAQ39149
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97.5	97.4	97.4	97.3	97.2	97.0	96.2	89.9	76.4	74.1	52.8	52.8	50.5	42.0	42.0	37.2	36.3	35.8	35.7	32.6	35.6	35.6	35.6	32.6	35.5	35.5	35.5	35.5	35.3	35.3	32.6	32.1	31.7	31.7	31.7	31.7
926	955.2	55.	954.6	923.6	952	943.8	882	749.4	727	518.4	517.8	495.8	412.2	412.2	365	356.2	351	350.4	349.4	349.4	349.4	349.4	349.4	348.2	348.2	348.2	348.2	346.6	346.6	319.8	315.2	311	311	m	310.8
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ALIGNMENTS

T 1 368 AAC91368 standard; DNA; 981 BP.	18;	2001 (first entry)	Modified human annexin nucleotide sequence, SEQ ID NO: 1.	!	Human; annexin; chelation site; nuclear imaging; apoptosis;	transplant rejection; ds.		piens.		3332-A1.	-	2000.		2000; 2000WO-US14324.		1999; 99US-0324096.	MOEDING MY FILME	ONIV WASHINGLOW.	, Brown DS;		01-080465/09.	AAB50863.	relinative market for important representation	odified annexin useful for imaging vascular thrombi
1 8 .C91368 standard;	AAC91368;	16-MAR-2001 (firs	dified human ann		man; annexin; ch	ansplant rejection	,	Homo sapiens.		WO200073332-A1.		07-DEC-2000.		25-MAY-2000; 2000W		01-JUN-1999; 99U	MOHOMERS AND A MINE A	TUCHA ATNO (MINI	Tait JF, Brown DS		WPI; 2001-080465/09.	P-PSDB; AAB50863.	modified spec	Novel modified ann
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                                     English.
                                     Page 28-30; 39pp;
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Best Local Similarity 99.8%; Pred. No. 6.6e-274;
Matches 979; Conservative 0; Mismatches 2;
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transplant rejection; ds.
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Pred. No. 1.9e-273;
0; Mismatches 3;
                                                                                                     Modified human annexin nucleotide sequence,
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Local Similarity 99.7%;
hes 978; Conservative (
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P-PSDB; AAB50865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rait JF, Brown DS;
                                                                                                                                                                                                                                                                                                     WO200073332-A1.
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Matches 978;
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71 AGCGGGCTGATGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGA 130
                                                                                                                                                               The vascular anti-coagulating protein (VAC)-alpha encoded by this cDNA is used in the preparation of monoclonal antibodies (WAbs). The VAC-alpha is injected into a host animal, in conjugation with egy keyhole limpet haemocyanin, and the B-cells from the immunised hosts are then fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-alpha. The Abs can be used as immunassay reagents to detect VAC proteins, as affinity ligands for purificn. of VACs and as medicaments for binding and/or neutralising VAC proteins in vivo. See also AAN91334 and EP-181465.

(Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                  GCATCCTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTT
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97.7%; Score 958.2; DB 10; Length 1466;
Best Local Similarity 99.2%; Pred. No. 4e-268;
Matches 963; Conservative 0; Mismatches 8; Indels 0;
                                                                                                             Monoclonal antibodies to vascular anti-coagulating proteins hybridomas producing such antibodies.
                                                                                                                                                                                                                                                                                                     Sequence 1466 BP; 423 A; 291 C; 327 G; 425 T; 0 other;
                                                                                                                                              Disclosure; flg 1; 11pp; German
                                 (BOEH ) BOEHRINGER INGELHEIM.
          88DE-3810331
                                                                            WPI; 1989-293724/41.
                                                                                       P-PSDB; AAP91953
          26-MAR-1988;
                                                       Gunther A;
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          ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATAT
                      GGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTG
                                                                                                                                                                                         TTTATCACCATCTTTGGAACACGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTAC
                                                                                                                                                                                                                                                                                                                                                 ACCUTCTATTATGCTATGAAGGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATG
                                                                                                                                                                                                                                                                                                                                                                      proteins; hybridomas; B-cells; myelomas;
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- Mus musculus
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10-MAR-2003
30-JUL-1989
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binding site, initiation sequence, termination codon and a transcription termination to the placental coagulation inhibitor gene. The polypeptide produced on culturing of transformed host cells exhibits strong anticoagulant activities and is useful for the treatment and prevention of eq thrombosis or disseminated intravascular coagulation in the brain, heart and peripheral blood vessels. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                              Length 1567;
                                region,
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                                                                                                                                                         Sequence 1567 BP; 430 A; 332 C; 358 G; 447 T; 0 other;
                                promoter
                                                                                                                                                                             .8; DB 9;
1.1e-267;
                                                                                                                                                                             Score 956.8; DB Pred. No. 1.1e-26
                                                                                                                                                                                                   0; Mismatches
                                sequence comprises a
           English.
                                                                                                                                                                             97.5%;
99.8%;
                                                                                                                                                                                                   958; Conservative
           ?; p;
                                                                                                                                                                                        Similarity
           Page
           Disclosure;
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TCTTTGGAACACGAAGTGTGTCTCATTTGAGAAGGTGTTTGACAAGTACATGACTATAT
           CAGGATTTCAAATTGAGGAAACCATTGACGGGAGACTTCTGGCAATTTAGAGCAACTAC
                                                 TCCTTGCTGTTGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGCCCTCTATT
                                                                                                                         ATGCTATGAAGGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGA
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                                                                                                      TCCTTGCTGTTGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation;
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136.1098
/*tag= a
/label-placental coagulation inhibitor
1568
                                                                                                                                                                                                                                                                                                                                                                                                                                     coagulation inhibitor; disseminated vascular
                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid contg. placental coagulation inhibitor gene
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87JP-0184428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1988-236733/34.
WPI; 1991-329110/45.
P-PSDB; AAP80511.
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JP03219875-A.
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10-MAR-2003
12-NOV-1990
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23-JUL-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombosis;
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This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially carpeased cDNAs in a sample. The cDNAs of the invention may have antiarteriosclerotic; cytostatic; cardiant; hypotensive, antidiabetic; gynaecological; vasotropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or more cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the movention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of creatment of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-eclampsia, ischaemia- repertusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new
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                                                                                                                                                 Human cDNA #162 differentially expressed in activated vascular tissue.
GGAGCTGGGACAGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT
                                                                        CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTTTTATTCCATGATT
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cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;
cerebroprotective; gene therapy; vascular disease; cancer; coronary;
artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
ischaemia-reperfusion injury; stroke;
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nucleic acid molecules. Antibodies to the proteins encoded by the CDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, embount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in activated vascular tissue.

Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic formet directly from USPTO at http.seqdata.uspto.gov/sequence.html?DocID=20020137081.
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Pred. No. 1.1e-267;
0; Mismatches 2; Indels 0;
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Best Local Similarity 99.8°
watches 958; Conservative
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99.8%; Pred. No. 1.1e-267;
11ve 0; Mismatches 2,
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/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; fig. 1; 13pp; English.
                                                                                                                                                                                                                                                                                                                           (RORE ) RORER INT OVERSEAS INC.
                                                                                         AAN91821 standard; DNA; 1605
                                                                                                                                                                                                                                                                                        89EP-0105626
                                                                                                                                                                                                                                                                                                         88US-0176802
                                                                                                                                                                           Placenta; blood coagulation
                                                                                                                                                         Endonexin II complete cDNA
                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 99.8
nes 958; Conservative
                                                                                                                                                                                             Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                             WPI; 1989-317181/44.
P-PSDB; AAP91021.
                                                                                                                                                                                                                                                                                                                                             Jaye M;
                                                                                                                                                                                                                                                                                        30-MAR-1989;
                                                                                                                                                                                                                                                                                                         31-MAR-1988;
                                                                                                                             25-MAR-2003
16-MAR-1990
                                                                                                                                                                                                                                                                     02-NOV-1989
                                                                                                                                                                                                                                                   EP339285-A
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Best Local Si
Matches 958;
                                                                                                                                                                                                                                                                                                                                             Kaplan R,
        982
                                                                                                           AAN91821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as a carrier molecule to build a thrombus-targeting thrombolytic fusion protein. The protein is the result of expression of a fusion gene (this sequence) comprising the Annexin V gene and a low-molecular urokinase gene, in insect cells. The Annexin V-scu-PA-32 fusion protein, expressed in insect cell strain Tn-5B1-4, has high affinity for active
                                                                                                                                                                    911 ATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCG
      CAGGATTTCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTAC
                           TCCTTGCTGTTGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATT
                                                                                                          GTGAGATTGATCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New thrombolytic fusion protein for targetting thrombus - fusion of Annexin V and urokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annexin V/urokinase fusion construct.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA11241 standard; DNA; 1803 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1575
                                                                                                                                                                                                      New DNA sequence encoding anticoagulant PP4 protein - and new recombinant protein, vectors, antibodies, etc., useful therapeutically and diagnostically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1575 BP; 461 A; 322 C; 351 G; 441 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                         DNA sequence encoding anticoagulant PP4 protein. inhibits blood coagulation at the thromboplastin The derived protein is 320 amino acids. (Updated on 25-WAR-2003 to correct PF field.) (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 956.6; DB 10
Pred. No. 1.2e-267;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                       Claim 1; table 1; 14pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.5%; 97.5%; 99.1%; p. 962; Conservative 0.11 Grove
88EP-0118039
                                        87DE-3737239
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                                                                                                                         Grundmann U, Abel KJ,
                                                                                 (BEHW ) BEHRINGWERKE
                                                                                                                                                                WPI; 1989-166767/23.
                                        03-NOV-1987;
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                                                                                  TGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGA
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                                        Gaps
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                         Length 1803;
and has the fibrinolytic activity of urokinase.
                                       5; Indels
             Sequence 1803 BP; 495 A; 415 C; 462 G; 431 T; 0 other;
                          DB 21;
                         Score 956; DB 21;
Pred. No. 2e-267;
0; Mismatches
                         97.5%;
99.5%;
                                      959; Conservative
                                Similarity
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thrombocytes
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                                                                                                                                                                                                                                                                                                            PAP-I; anticoagulant; anti-inflammatory agent; phospholipid; phospholipase A2; disseminated intravacular coagulation; human placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human proteins having anticoagulant and antiinflammatory activity -
isolated from biological fluid by anion-exchange chromatographoc media.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAP-I cDNA from human placenta, used for anticoagulant production
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Pred. No. 3e-267;
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                                                                                                              AAN82107 standard; cDNA; 1454
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                                                                                                                                                                                                                                                                                                                                                          deep vein thrombosis; ss.
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                                                                                                                                                                                                                                                         DNA sequences encoding hybrid phospholipid-binding proteins (PBP) comprising at least one lipocortin phopholipid binding domain (PBD), e.g. of PAP-I, joined to a gla-domainless vitamin K-dependent protein, e.g. protein C or activated protein C. See AAQ12680-81 for such examples. A human placenta cDNA library was screened using affinity-purified antibody against PAP-I in order to obtain this cDNA. (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                  This sequence, or a fragment of it, is used in the construction
                                                                                                                                                                                                                                                                                                                                                                              Length 1460;
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                                                                                                                                                                                       Recombinant prodn. of hybrid phospholipid-binding proteins comprising lipocortin phospholipid-binding domain and vitamin K-dependent protein
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Matches 957; Conservative
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                                                                                             ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT
                                                                                                                                                                                                                               Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha
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Adolf G, Reutlingsperger CMP;
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vascular anti:coagulating proteins -
iul as thrombin inhibitors, antiflammatory agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 954.6; DB 9;
Pred. No. 4.5e-267;
0; Mismatches 4;
                                                                German.
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                                                             Disclosure; Fig 4/1-4/3; 183pp;
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milarity 99.6%; P
Conservative 0;
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              GGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA
                                                                         TCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGAT
                                                                                                       TAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGA
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                                                                                                                                                                     Score 953.6; DB 9;
Pred. No. 7.2e-267;
0; Mismatches 4;
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les 956; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lipocortin-V was isolated from a lambda gtl0 human peripheral blood lymphocyte cDNA library with rat lipocortin-V cDNA of lambda RLipo V-1 as probe. Lipocortins are anti-inflammatory agents and can be used to treat arthritic, allergic, dermatologic, ophthalmic, and collagen diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                    Human lipocortin cpds. III, IV, V, and VI - used in treatment of arthritic, allergic, dermatologic, ophthalmic and collagen disorders involving inflammatory processes.
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                                                                                                                                                                           Human lipocortin-V; lambdaRLipo V-1; anti-inflammatory agent.
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Pred. No. 2.7e-266;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also AAP91362, AAN90598, and AAP91363.
                                                                                                                                                                                                                                                                                                                                                                     Browning JL;
                                                                                                                                                                                                                   Location/Qualifiers
complement (143..1102)
/*tag= a
                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; fig 4; 32pp; English.
                                                                                          AAN90599 standard; cDNA; 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 97.0%; al Similarity 99.5%; 955; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     Pepinsky RB,
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                                                                                                                                                                                                                                                                                                                                              (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAP91363.
                                                                                                                                                                                                                                                                                                                          26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                 Wallner BP,
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593 GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCCTTCAGGCTAAC 652

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                                                                                                                                                                                                                                                                                                                                                                                                                 associated proteins represented in AABS106 - AABS18548. Lung cancer associated proteins represented in AABS106 - ABS18548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antegonists may have neuroprotective; cytostatic; cardioactive; and munomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the polynucleotide sequences. The lung cancer associated polynucleotide sequences. The lung cancer associated polynucleotide sequences. The protein of lung cancer, chromosome identification, as chromosome markers, and for numerous other disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative infectious diseases. Polynucleotide sequences AAF18435 and refectious diseases. Polynucleotide sequences AAF1845. - AAF18433 and peptide AABS8549 are used in the course of the invention for the course of the infectious diseases.
                                                                                                                                                                                                                                                                 Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                          cancer
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                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 746; 1425pp; English.
08-MAR-2000; 2000WO-US05918.
                                            99US-0124270.
                                                                                                                                                                                                WPI; 2000-587514/55.
P-PSDB; AAB58393.
                                                                                     (HUMA-) HUMAN GEN(
(ROSE/) ROSEN C A.
                                            12-MAR-1999;
                                                                                                                                                         Ruben SM;
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Sequence 1637 BP; 455 A; 349 C; 378 G; 450 T; 5 other;

Ouery Match

Best Local Similarity 99.6%; Pred. No. 6.6e-264;

Matches 956; Conservative 0; Mismatches 3; Indels 1; Gap

GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 141 ATTGTGGCTCTGAAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG 321 413 ATTGTGGCCTCTGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG 472 AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA 381 GTGGTGGGGACACTTCAGGGTACTACCAGGGATGTTGGTGGTTCTCCTTCAGGCTAAC 501 AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT GAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC 1; Gaps Local Similarity 99.6 nes 956; Conservative 82 233 142 293 262 322 382 442 Best Loca Matches g ò a g ò g a ð ö Š 8 ð

PAGAGACCCTGATGCTGGAATTGATGATGAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561	2 CAGGCTGGAGAACTTAAATGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA 621 	CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 681 	9 ATTGAGGAAACCATTGACCGCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT 741	9 GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGACCCTCTATTATGCTATGAAG 801 	9 GGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT 861 	CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATT 921	922 AAGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCCTCCGGAGAAGATGAC 981
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Search completed: August 28, 2003, 16:03:33 Job time : 220.333 secs

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August 28, 2003, 15:49:00; Search time 55.3333 Seconds (without alignments) 7825.244 Million cell updates/sec
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1 atggcatgtggctgcggtca.....tgctctccggagaagatgac 981
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2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptcdata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptcdata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                            OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 5, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 261, Appl Sequence 261, Appl Sequence 261, Appl Sequence 261, Appl Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 721, Appli Sequence 625, Appl Sequence 625, Appl Sequence 625, Appl Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 20, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 11, Appli Sequence 113, Appli	
SUMMARIES	US-09-324-096A-5 US-09-324-096A-3 US-09-324-096A-3 US-09-324-096A-3 US-08-125-746-2 US-08-125-746-4 US-09-480-884A-261 US-09-543-59-261 US-09-543-59-261 US-09-620-318-31 US-09-620-318-31 US-09-328-111-625 US-09-620-318-111-491 US-09-328-111-428	
DB	4446HH4444WW4WWW4WW44H444	
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Pred. No. 2.1e-283;
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TITLE OF INVENTION: METHODS FOR PRODI
POPPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,07/459,082
FILLING DATE: 29-DEC-1989
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LENGTH: 1460
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Pred. No. 1.9e-289;
0; Mismatches 3;
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH E FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 981
                                                                                                                                                                          99.5%;
llarity 99.7%;
Conservative
                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (1)..(981)
US-09-324-096A-3
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                                                                                                                          Length 1567;
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                                                                                                                         Score 956.8; DB 1;
Pred. No. 2.1e+283;
0; Mismatches 2;
                         TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                          97.5%;
99.8%;
                                                                                                                                                      Conservative
               unknown
                                                                  CDS
136..1095
nucleic acid
                                                                                                                    Query Match
Best Local Similarity
Matches 958; Conserv
              STRANDEDNESS:
                                                                HAME/KEY:

COCATION:

US-08-125-746-2
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           CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA
                           GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGCCCTCTATTATGCTATGAAG
                                                                                                                                                                                             GGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT
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: 1755 S. Jefferson Davis Highway, Suite 400
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDJUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATE: DO 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION NUMBER: US 184428/1987
FILING DATE: 23-JUL-1987
ATPONREY/AGENT INPOMATION:
NAME: Oblon, NO: 5591633man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SAINO, YUSHI
APPLICANT: IMASAKI, AKIO
APPLICANT: INASAKI, AKIO
APPLICANT: SUDA, MAKOTO
ITILE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIV
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REFERENCE/DOCKET NUMBER: 80-074-0 |
TELECOMMUNICATION INFORMATION:
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Patent No. 5591633
GENERAL INFORMATION:
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TELEFAX: (703) 413-3200
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 here
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CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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                264
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                                                                                        GGAGCTGGAACAAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAAGAA
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                               301 GGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAAGAA
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                  GTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTGAAG
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APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND
TITLE OF INVENTION: AND DIAGNOSIS OF
FILE REFERENCE: 210121.455C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 261, Application US/09643597
Patent No. 6426072
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aljun
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Fan, Liqun
Kalos, Michael D.
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APPLICANT:
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               AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTGCTCCGGAGAGATGAC 981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                               ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 953.8; DB 1;
Pred. No. 1.4e-282;
0; Mismatches 2;
                                                                                                                                   MEKAL INFORMATION, VUSHI
APPLICANT: SAIDO, VUSHI
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NIMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Oblon, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-ULL-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               Sequence 4, Application US/08125746
Patent No. 5591633
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y: unknown
TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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99.8%;
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 955; Conserv
                                                                                                                                                                                                                                                                                         Virginia
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TOPOLOGY: unk
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                      RESULT 6
US-08-125-746-4
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329 ATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG 388
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                                                                                                                                                                                 89 ATGGCACAGGGTTCTCAGAGGCACTGNGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT
                      22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT
                                                                                           82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGGAGCATCCTGACT
                                                                                                              82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCCACAGATGAGGAGCATCCTGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fan, Salos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Banger, Gary R.
APPLICANT: Fornger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN FILE REFERENCE: 2012.1455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILLING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 261, Application US/09542615A Patent No. 6518256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(401); OTHER INFORMATION: n = A,T,C or G US-09-542-615A-261
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Best Local Similarity 99.4%;
Matches 311; Conservative (
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389 AAGGGAGCTGGAA 401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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LENGTH: 401
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                                                                                                                                                                                                                                                    Length 401;
                                                                                                                                                                                                                                                  Query Match 31.7%; Score 311; DB 4; Length 40
Best Local Similarity 99.4%; Pred. No. 1.2e-85;
Matches 311; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 261
LENGTH: 401
              CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 261
LENGTH: 401
CURRENT APPLICATION NUMBER: US/09/643,597 CURRENT FILING DATE: 2000-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 261, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
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NAME/KEY: mlsc_feature

LOCATION: (1)...(401)

OTHER INFORMATION: n = A,T,C or G
US-09-480-884A-261
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! LOCATION: (1)...(401)

! OTHER INFORMATION: n =

US-09-643-597-261
                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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Best Local Similarity
Matches 311; Conserv
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT PELICATION UNDERS: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.7%; Score 311; DB 4;
Best Local Similarity 99.4%; Pred. No. 1.2e-85;
Matches 311; Conservative 0; Mismatches 2
                                                                                                                                                         Sequence 261, Application US/09606421B Patent No. 6531315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) NAME/KEY: misc_feature

) LCCATION: (1)...(401)

) CTHER INFORMATION: n = A,T,C or G

US-09-606-421B-261
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                                                                                                                                                                                                                                    Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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                                                       322 AAGGGAGCTGGAA 334
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APPLICANT: WANG, TONGTONG
APPLICANT: Fan, Liqun
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                                                                                                                                                US-09-606-421B-261
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APPLICANT:
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                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 558X
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
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                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATONNEY/AGENT INFORMATION:
RAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                            et
GENERAL INFORMATION:
APPLICANT: TOWLE, Christine A.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                        3: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION IRRORAMTION: TELEPHONE: (617) 542-8970
TELEPRAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                        Massachusetts
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US-08-526-136-1
                                                                                                                                                                                                                ZIP: 02110-2804
                                                                                                                            STREET: 225 F1
CITY: Boston
STATE: Massacl
COUNTRY: U.S.A
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                                                                                                 205 CCGCCTGGGAACAGATGACCAAGTTCAATGCGATTCTGTGCTCCCGGAGCCGGGCCCA 1264
                                                                                                                                                                                                                                        695
                                                                                                                                                                                                                             696 TGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTTGTGAAATCTATTCG 755
                                   456 ITCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAACAGAGACCCTGATGC
                                                                                 516 TGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACT
                                                                                                                                576 TAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACACGAAGTGTGTCTCA
                                                                                                                                                                               636 TTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAAATTGAGGAAACCAT
                                                                                                                                                                                                                                                                                                                          816 TGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGATCTGTTTAACATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    936 TGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDUUW TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordberfect (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Towle, Christine A. et
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08526136
Patent No. 6107089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
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STATE: Massachusetts
COUNTRY: U.S.A.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Pred. No. 3.3e-85;
0; Mismatches 397;
| RECISTRATION NUMBER: 30,162 | REFERENCE/DOCKET NUMBER: 00786/099001 | TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 | TELEFAX: (617) 542-8906 | INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2311
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.0%;
Matches 549; Conservative
                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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1302 TACCAAGTCCTGATTCGCATCCTTATCTCTCGATGTGAGACTGACCTTCTGAGTATCAGA
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                                                        GAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAA
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APPLICANT: Burges, Christopher C.
APPLICANT: Busheell, Steven E.
APPLICANT: Carroll III. Eddle
APPLICANT: Catrol, Theodore J.
APPLICANT: Catrol, Theodore J.
APPLICANT: Catrol, Theodore J.
APPLICANT: Lewis, Marcia E.
APPLICANT: Honahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION: PRODUCTS
TITLE OF INVENTION NUMBER: US/09/328,111
CURRENT APPLICATION NUMBER: US/09/38,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER PILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
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Patent No. 6262333
GENERAL INFORMATION:
APPLICAMT: Endege, Wilson O.
APPLICAMT: Steinmann, Kathleen E.
APPLICAMT: Astle, Jon H.
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                                                                                                                 Indels
                                                                                          TGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC
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Pred. No. 3.1e-31;
0; Mismatches 479;
                                                                                                                                                                                                                              Sequence 747, Application US/09620312D Patent No. 6569662
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John Tillinghast
Drmanac, Radoje
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
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Best Local Similarity 48.0
Matches 454; Conservative
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Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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Ma, Yunging
Wang, Dunrui
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; LOCATION: (435)..(1472)
US-09-620-312D-747
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FEATURE:
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                                                                                                                                                           Length 644;
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, John H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Cotino, Theodore J.
APPLICANT: Lewis, Marcia E.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE COP-257 (US)
FILE REFERENCE: CCO-257 (US)
                                                                                                                                                         Score 123.6; DB 3; Length
Pred. No. 4.3e-28;
0; Mismatches 241; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 721 LENGTH: 644
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Patent No. 6262333
                                                                                 NAME/KEY: misc_feature

LCCATION: (1)...(644)

CTHER INFORMATION: n = A,T,C or G

US-09-328-111-721
                                                                                                                                                        tch 12.6%; sal Similarity 52.6%; 267; Conservative
                                           TYPE: DNA
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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Best Local
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                                                                       FEATURE:
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Pred. No. 7.2e-20;
0; Mismatches 174;
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: August 28, 2003, 19:41:19 Job time : 57.3333 secs
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                                                                                                                                                                                                                                                                Query Match . 9.81
Best Local Similarity 53.65
Matches 201; Conservative
                                                                                                                                            LENGTH: 502
TYPE: DNA
CRGANISM: Homo sapiens
US-09-328-111-625
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August 28, 2003, 15:49:00; Search time 55.333 Seconds (without alignments) 7825.244 Million cell updates/sec
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1 atggcatgtggcggtggcca......tgctctccggagaagatgac
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                  569978 seqs, 220691566 residues
                                                                      - nucleic search, using sw model
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* Issued_Patents_NA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 1, Appli Sequence 3, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 261, Appli 20, 7 14, 7 123, 106, Description Sednence Sed US-08-125-746-2 US-08-125-746-4 US-09-643-597-261 US-09-643-597-261 US-09-542-615A-261 US-09-542-615A-261 US-09-526-136-3 US-09-526-136-3 US-09-328-111-721 US-09-328-111-491 US-09-328-111-491 US-09-328-111-491 US-09-328-111-491 US-09-328-111-491 US-09-328-111-491 US-09-328-111-491 US-09-325-932A-17 US-09-324-096A-1 US-09-324-096A-3 US-09-324-096A-5 US-09-641-638-123 US-09-641-638-106 US-09-641-638-107 -09-328-111-428 -09-325-932A-21 SUMMARIES Length 23305 2311 1793 644 644 630 502 643 643 643 704 7001 1001 1001 Query Match 1 0000 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 09090 Score Result No. U 0000 U

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24, Apr 126, Apr 126, Apr 126, Apr 126, Apr 126, Apr 126, Apr 1270, Apr 1270	SITES	Gaps	TTCCCT SGCACA 11111
sedaneu ce sedaneu ce	CHELATION	Length 981; Indels 0; GCACTGTGACTGACT	
US-09-451-651-24 US-08-594-031-156 US-09-641-638-81 US-09-641-638-202 US-09-641-638-201 US-08-961-083-33 US-09-535-78-108 US-08-961-527-108 US-08-961-527-108 US-08-454-557C-101 US-08-450-101 US-08-450-101 US-08-252-991A-5409 US-09-252-991A-5404 US-09-252-991A-5404 US-09-252-991A-5404	ALIGNMENTS 1096A. RIVATIVE WITH ENDOGEN 31	100.0%; Score 981; DB 4; Length 981; inilarity 100.0%; Pred. No. 8.3e-284; Conservative 0; Mismatches 0; Indels 0; Gaps ATGGCATGGCGGTGGCCATATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCT	
4H444W44W40W0444444	09324 N DER + 1 - 06-0 3.0	100.0%; 100.0%; ive (GGTGGCC)	
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$\frac{1}{2} \frac{1}{2} \frac{1}$	1, Application US/(5.632313) INFORMATION: INFORMATION: WR: Talt, Jonathan WR: Brown, David F INVENTION: ANNEXI FERENCE: UOFW-1-138, FILING DATE: 1999 FILING PATE: 1999 FILING	Similarity 1; Conser ATGGCATGT	IIIIIII IGGCATGI SATTIGAI SATTIGAI
444 44 44 44 44 44 44 44 44 44 44 44 44	RESULT 1 Sequence 1, Application US/09 Patent No. 6213313 GENERAL INFORMATION: APPLICANT: Tait, Jonathan APPLICANT: Brown, David TITLE OF INVENTION ANNEXIN CURRENT FILLS UCFW-1-1341 CURRENT FILLING DATE: 1999-0. CURRENT FILLING DATE: 1999-0. NUMBER OF SEQ ID NOS: 12 SOFTWARE: PatentIN version 3 SEQ ID NO 1 LENGTH: 981 TYPE: DNA ORGANISM: HOMO Sapiens FEATURE: NAME/KEY: CDS LOCATION: (1)(981)	atch cal S 981	1 A' 61 G(61 G(
80000000000000000000000000000000000000	SULT 1 -09-324-09 Sequence 1 Sequence 1 Septent No. GENERAL IN TITLE OF FILE REPERT OF CURRENT A CURRENT A CURRENT A CURRENT A CURRENT A CURRENT B CURRENT	Query M Best Lo Matches	
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Oy 361 ATTGCTTCAAGGACACCTGAAGAGCCATCAAACAAGTTATGAAGAATAT 420	Db 421 GGCTCAAGCCTGGAAGATGACGTGGGGGAACTTCAGGGGTACTACCAGCGGATGTTG 480 Qy 481 GTGCTTCTTCAGGCTAACAGAGACCCTGATGCTGGAATTGATGATGATGATGAAGTTGAA 540 Db 481 GTGCTTCAGGCTAACAGAGACCCTGATGCTGGAATTGATGAAGTTGAAGAGTTGAA 540	541 CAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAGG IIIIIIIIIIIIIIIIIIIIIIIIIIIII	TTGACAAGTAC 6	661 ATGACTATATCAGGATTTCAAATTTATATATCAATTTATTT	781 ACCCTCTATTATGCTATGAAGGGAGCTGGGACAGATGATCATCATCCTCATCAGAGTCATG	941 GITTCCAGGAGTGAGTTGATCAGGAGGAGTTTAGGAAGAGTTTTAGCC 9 841 GITTCCAGGAGTGAGATTGATCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCC 9 901 ACCTCTCTTATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTG 9	- S	RESULT 2 US-09-324-096A-3 ; Sequence 3, Application US/09324096A ; Patent No. 63233333 ; Patent ANDOMATION	CONTROL IN CONTROL OF TAIL, JOHATHAN APPLICANT: Brown, David TITLE OF INVENTION: MINEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES TITLE OF INVENTION: MINEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES		C)	S-0	Query Match Best Local Similarity 99.7%; Score 977.8; DB 4; Length 981; Best Local Similarity 99.8%; Pred. No. 7.5e-283; Matches 979; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 1 ATGCATGTGGCGGTGGCATATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCT 60

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13 ATGGCACAGGTTCTCAGAGGCACTGTGACTTGACTTCCCTGGATTTGATGAGGGGGTGAT
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es 2;
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Pred. No. 1.8
                                                                                                                                                          APPLICANT: FOSTER, DONALD
TITLE OF INVENTION: METHODS FOR PRODI
PHOSPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/459,082
FILING DATE: 29-DEC-1989
                                                                                          CTGCTCTCCGGAGAAGATGAC 981
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Matches 958
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Pred. No. 2.3e-282;
                                                                                                                                                    Mismatches
        DERIVATIVE WITH
     TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH
FILE REPEBENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 5
LENGTH: 981
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                                                                                                                                  99.58;
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Best Local Similarity 99.7
Matches 978; Conservative
Brown, David
                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                        FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(981)
US-09-324-096A-5
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                                                                                                                   Length 1567;
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                                                                                                                   Score 956.8; DB 1;
Pred. No. 1.8e-276;
0; Mismatches 2;
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0
                        TOPOLOGY: 'unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                   97.5%;
                                                                                                                                            Conservative
             unknown
                                                                CDS
136..1095
nucleic acid
                                                                                                                               1 Similarity
958; Conserv
TYPE: nucleic
STRANDEDNESS:
                                                                ; NAME/KEY:
; LOCATION:
US-08-125-746-2
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     ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24.5EP-1993
CLASSIPICATION: 530
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 037227/1987
FILING DATE: 20.FEB-1987
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APPLICANT: IWASAKI, AKIO
APPLICANT: IWASAKI, AKIO
APPLICANT: SUDA, WAKOTO
ITILE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, WAIER
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Oblon, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/COCKET NUMBER: 00-074-0
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08125746
Patent No. 5591633
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELER: 248855 OPAT UR
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                   GTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTGAAG
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APPLICANT: MCNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND ITILE OF INVENTION: AND DIAGNOSIS OF PILE REFERENCE: 210121.455C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 261, Application US/09643597 Patent No. 6426072
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
Panger, Gary R.
Li, Samuel X.
Wang, Aijun
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APPLICANT:
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APPLICANT:
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 AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC
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                                                                                                                                                                                                                                                     MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                 APPLICANT: SAINO, YUSHI
APPLICANT: SAINO, YUSHI
APPLICANT: SAINO, WAKOTO
APPLICANT: SUDA, WAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUST
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 953.8; DB 1;
Pred. No. 1.1e-275;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                           #1.25
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION NUMBER: UP 037227/1987
FILING DATE: 20-FEB-1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-ULL-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80-074-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Oblon, No. 5591633man F. REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074
TELECOMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                        Sequence 4, Application US/08125746
Patent No. 5591633
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
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|larity 99.8%;
|Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 957 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Raios, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 3.0
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8.09-542-615A-261
7 Sequence 261, Application US/09542615A
7 Patent No. 6518256
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COTHER INFORMATION: n = A,T,C or US-09-542-615A-261
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SEQ ID NO 261
LENGTH: 401
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APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 261
LENGTH: 401
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 261, Application US/09480884A Patent No. 6482597
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)...(401)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(401)

OTHER INFORMATION: n = A,T,C or G

US-09-643-597-261
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Best Local Similarity 99.4
Matches 311; Conservative
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US-09-480-884A-261
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
SOFTWARE: FastESQ for Windows Version 3.0
SEQ ID NO S: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 401;
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                                                                                                                                         Sequence 261, Application US/09606421B Patent No. 6531315 GENERAL INFORMATION:
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NAME/KEY: misc_feature

LOCATION: (1)...(401)

OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-261
                                                                                                                                                                           APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
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Best Local Similarity 99.4%;
Matches 311; Conservative
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ORGANISM: Homo sapien
                                                                                                                     RESULT 10
US-09-606-421B-261
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US-08-526-136-1
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                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER PEDS BEFORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WORDPETECT (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE_POCKET NUMBER: 00786/099001
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-806
TELEPHONE: (617) 542-806
TELER: 200154
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATORNEY/AGENT INFORMATION:
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             APPLICANT: Towle, Christine A. e
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 58.0
Matches 549; Conservative
                                                                                                                                               Massachusetts
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STRANDEDNESS: single
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US-08-526-136-1
GENERAL INFORMATION:
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                                                                                                                                             STATE: Ma
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Query Match
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1025 GAACAGAGTCTACAAGACAGAATTCAAAAAGACCCTGGAGGAGGCCATTCGGAGCGACAC 1084
                                                                                                                                                                                                                                                          696 TGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTTGTGAAATCTATTCG 755
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                                                                                   516 TGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACT
                                                                                                                                            576 TAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACACGAAGTGTGTCTCA
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CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5° Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
COMPUTER: WordPerfect (Version 5.0)
COMPUTER: MOTGPerfect (Version 5.0)
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FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08526136 Patent No. 6107089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: TOWLE, CHISTINE A.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2: Fish & Richardson
225 Franklin Street
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 22
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                                                                                                                                                                                                                                                                  Length 2311;
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                                                                                                                                                                                                                                                                                                        Mismatches 397;
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                                                                                                                                                                                                                                                                    Score 310.8;
                   00786/099001
                                                                                                                                                                                                                                                                                          Pred. No
                                                                                                                                                                                                                                                                                                          ö
REGISTRATION NUMBER: 30,162
                   REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-6570
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                    31.7%;
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Matches 549; Conservative
                                                                                           TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       ; TYPE: nucleic acid
; STRANDENESS: single
: TOPOLOGY: linear
US-08-526-136-3
                                                                                                                                                       LENGTH: 2311
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1362 GCTGAGTTCAGGAAGAATTTGGGAAGTCCCTCTACTCTTCTCTCCAGGATGCAGTGAAA 1421
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697 GACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTTGTGAAATCTATTCGA 756
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                                                                                                 GTGGACGTGGCCATTGAAATTCTTGCCACTCGAACCCCACCCCAGCTGCAGGAGTGCCTG
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                                                            GAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAA
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burges, Christopher C.
APPLICANT: Busnell, Steven E.
APPLICANT: Cartiol III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Catino, Theodore J.
APPLICANT: Catino, Theodore J.
APPLICANT: Catino, Macia E.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
TILE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION NUMBER: US/09/328,111
CURRENT FILIKG DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-10
NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               937 GGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC 981
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                 876 GAAGGAGTTTAGGAAGAATTTTGCCACCTCTTTTATTCCATGATTAAGGGAGATACATC 935
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                                                                                                                         936 TGGGGACTATAAGAAAGCTCTTCTGCTGCTCCCGGAGAAGATGAC 981
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TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: No. 656962el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PELL genes Version 1.0
SEQ ID NO 747
LENGTH: 1793
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48.0%; Pred. No. 2.3e-30;
tive 0; Mismatches 479;
                                                                                                                                                                                                                                           Sequence 747, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wehrman, Tom
Xue, Aldong J.
Yang, Yonghoog
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                      APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 48.0
Matches 454; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (435)..(1472)
US-09-620-312D-747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                                                                                                                                                               Length 644;
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Barle, Jon H.
APPLICANT: Burges, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Catroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                             Score 123.6; DB 3;
Pred. No. 2.7e-27;
0; Mismatches 241;
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 721
LENGTH: 644
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Patent No. 6262333
GENERAL INFORMATION:
                                                                                                                 NAME/KEY: misc_feature

LOCATION: (1)...(644)

COTHER INFORMATION: n = A,T,C or G

US-09-328-111-721
                                                                                                                                                                                                            Query Match 12.6%;
Best Local Similarity 52.6%;
Matches 267; Conservative
                                                                                ORGANISM: Homo sapiens
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                                                               TYPE: DNA
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9.8%; Score 96.6; DB 3;
Best Local Similarity 53.6%; Pred. No. 2.9e-19;
Matches 201; Conservative 0; Mismatches 174;
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 625
LENGTH: 502
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US-09-328-111-625
                                                                                                                     LENGTH: 50
TYPE: DNA
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7825.244 Million cell updates/sec
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                                                                                                                                                                                            August 28, 2003, 15:49:00 ; Search time 55.3333 Seconds
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Sequence 5
Patent No.
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1-09-542-615A-261
1-09-606-421B-261
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US-08-125-746-4
US-09-64-597-261
US-09-64-51-261
US-09-66-4218-261
US-08-526-136-3
US-08-526-136-3
US-09-53-131-721
US-09-328-111-721
US-09-328-111-491
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Maximum Match 100%
Listing first 45 summaries
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US-09-451-651-24 US-08-594-031-156 US-09-641-638-81 US-09-641-638-202 US-09-641-638-202 US-09-641-638-202 US-08-961-083-33 US-08-961-083-33 US-08-961-083-33 US-08-961-083-33 US-08-454-557C-101 US-08-454-557C-101 US-08-454-577C-101 US-09-101-101 US-09-101111A-101 US-09-101-101 US-09-252-991A-5401 US-09-252-991A-5409 US-09-252-991A-5409 US-09-252-991A-5409 US-09-252-991A-5409 US-09-252-991A-5409 US-09-252-991A-5409	ALIGNMENT	IVE 24,0		core 981; red. No. 1. Mismatches	GCAC	GAAA 	TTGA	98CA	6766 	GGAG GGAG
	AL	096A IVAT 19/3		ω m.	TATG TATG	TGCA TGCA	TCTG - - TCTG	GTTT	AATT 	GAAG GAAG
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8000HREEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE		ULT 09-3 99-3 equel energappi FITE CURRI CURRI SOFTW	SEQ ID LENGI TYPE: ORGAN FEATU NAME, LOCA1	Query Match Best Local Matches 98						
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Db 1 ATGGCATGTGGCGGTGGCCATATGGCACGGTTCTCAGAGGCACTGTGACTTCCCT 60 GGATTTGATGACGGCTGATGCAGAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120	181 181 241	Db 241 ACTGGAAATTGAAAATTGTGGCTCTGATGAACCCTCTCGGCTTTATGATGT 300 Qy 301 TATGAACTGAAACATGCCTTGAAGGGACGACAAAAGAAAAAGTACGAAAATT 360 Db 301 TATGAACTGAACATGCCTTGAAGGGACGAACAAAAGTACTGACAAAATT 360 Qy 361 ATGCTTCAAGGACCTGAAGAACTGAAGAATATAAGAAAAAAT 420	Db 361 ATTGCTTCAAGGACCCTGAAGGACCCATCAACAAGATTTTATGAAGAAGATT 420 Oy 421 GGCTCAAGGAGAGTGACGGGGGACACTTCAGGGTACTACCAGCGGATGTT 6 480 Db 421 GGCTCAAGCCTGGAAGATGACGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTG 6 80 Oy 481 GGCTCAAGCCTGGAAGATGACGTGGTGGGAACTTCAGGGTACTACCAGCGGATGTTG 480 Oy 481 GTGGTTCTCCTTCAGGCTAACAGAGACCCTGATGGAATTGATGAAGGTCAAGTTGAA 540	481 GIGGTICTCCTTCAGGCTAACAGAGACCTGATGCTGGAATTGATGAAGCTCAAGTTGAA 541 CAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTTGAAGTGAAGAA	Oy 601 TTTATCACCATCTTGGAACACGAAGTGTCTCATTTGAGAAAGGTGTTTGACAAGTAC 660	OY 721 GAGCAACTACTCCTTGCTGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGGG 780	OY 841 GTTTCCAGGAGTGAGATTGATCTGTTTAACATCAGGAGGAGGTTTAGGAAGAATTTTGCC 900 B41 GTTTCCAGGAGTGAGATTGATCTTTTAACATCAGGAAGGA	961 CTGCTCTCCGGAGAGATGAC 981 	RESULT 3 US-09-324-096A-5 Sequence 5, Application US/09324096A ; Sequent No. 6323313 ; GENERAL INFORMATION: ; APPLICANT: Talt, Jonathan
Qy 361 ATTGCTTCAAGGACACCTGAAGAACTGAGGCCATCAAACAAGTTTATGAAGAATAT 420 Db 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAATAT 420 Qy 421 GGCTCAAGCCTGGAGGAGGCGTCATCAGGGTACTACCAGCGGATGTTG 480 Db 421 GGCTCAAGCCTGGAGGAGGACACTTCAGGGTACTACCAGCGGATGTTG 480 C 1		Oy 601 TTTATCACCATCTTGGAACACGAAGTGTCTCATTTGACAAAGGTGTTTGACAAGTAC 660 Db 601 TTTATCACCATCTTTGGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTAC 660 Oy 661 ATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACGGGAGACTTCTGGCAATTA 720 Db 661 ATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACGGGGAGACTTCTGGCAATTA 720	OY 721 GAGCAACTACTCGTGTTGTGAAATCTATTGGAAGTATACCTGCCTACCTTGCAGGG 780		CTCTCTTATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGGGCCTTATAAGAAAGGGCCTTTATAAGAAAGGGCCTTTATAAGAAAGGGCACTTATAAGAAAGGGCACTTATAAGAAGATACATCCGGGAGAAGATGAC 981	ស៊ីស្លេក្ល	File Kerekence: UOFW-1-13841 CURRENT APPLICATION UNBER: US/09/324,096A CURRENT FILING DATE: 1999-06-01 NUBBER OF SEQ ID NOS: 12 SOFWARE: Patentin version 3.0 SEQ ID NO 1 TENGTH: 981	ORGANISM: Homo sapiens FEATURE: FEATURE: LOCATION: (1)(981) 5-09-324-0968-1	Ouery Match Ouery Match Best Local Similarity 99.8%; Pred. No. 1.3e-282; Matches 979; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Oy 1 ATGGCAGGTGGCCATATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCT 60

	RESULT 4 522557-3 ; Patent No. 5225537 ; Patent No. More Poly Patent No. 5225537 ; APPLICANT: FOSTER, DONALD ; TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID ; PHOSPHOLIPID-BINDING PROTEINS ; NUMBER OF SEQUENCES: 14 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/07/459,082 ; SEQ ID NO:3: LENGTH: 1460 5225537-3	Ouery Match 97.5%; Score 956.8; DB 6; Length 1460; Best Local Similarity 99.8%; Pred. No. 3e-276; Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Oy 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCTTCCCTGGATTTGATGAGGGGTGAT 81	142 CTGTGACACTCTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAAGCATCTGACT 1 142 CTGTGACATCCCGAAGTAATGCTCAGGGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 2 1142 CTGTTGACATCCCGAAGTAATGCTCAGGGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 2 1143 CTGTTGACATCCCGAAGTAATGCTCAGGGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 1 202 TTTGGCAGGATCTTCTGGATGACCTGAAAATTA 2	Db 193 TTTGGCAGGATCTTCTGGATGACCTGAATCAGAACTAACT	373 GAACTGGGGGACACTAAAAAAGAAGAAAAAAAAAAAAAA
APPLICANT: Brown, David TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES: FILE REFERENCE: U0FW-1-13841 CURRENT APPLICATION NUMBER: U5/09/324,096A CURRENT FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.0 SEQ ID NO 5 LENGTH: 981 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS LOCATION: (1).(981) US-09-324-096a-5	Query Match 99.5%; Score 976.2; DB 4; Length 981; Best Local Similarity 99.7%; Pred. No. 3.9e-282; Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0; QY 1 ArGGCAGGTGGCCCATANGGCACGGTTCTCAGAGGCACTGTGACTTCCCT 60 111111111111111111111111111111111111		301 TATGAACTGAACATGCCTTGAAGGGAGCTGGAACAATGAAAAGTACTGACAGAATT 3 11111111111111111111111111111111111	0y 421 GGCTCAAGCCTGGAAGATGACGTGGGGACACTTCAGGGTACTACCAGCGGATGTTG 480 1 1 1 1 1 1 1 1 1 1	601 TTATCACCATCTTGGAACACGAGTGTCTCATTGAGAAAGGTGTTTGACAAGTACTACTACTACTACTACTACTACTACTACTACTACTACT

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                                                                                                   Length 1567;
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                                                                                                  Score 956.8; DB 1;
Pred. No. 3.1e-276;
0; Mismatches 2;
                     TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
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nucleic acid
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Best Local Similarity
Matches 958; Conserv
           STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                       MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1755 S. Jefferson Davis Highway, Suite 400 STATE: Virginia COUNTRY: U.S. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SAINO, YUSHI
APPLICANT: IMASAKI, AKIO
APPLICANT: SUDA, MAKOTO
APPLICANT: SUDA, MAKOTO
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Oblon, No. 5591633man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 037227/1987
FILING DATE: 20-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08125746 Patent No. 5591633 GENERAL INFORMATION:
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TELEX: 24855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1567 No.
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                                   325 GGAGCTGGAACAAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAAGAA
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APPLICANT: McMeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
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Patent No. 6426072
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Hosken, Nancy
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Skeiky, Yasir A.W.
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Fan, Liqun
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Li, Samuel X.
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APPLICANT: Wang, T
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                                                                                                                                                                                                                                                                   E: P.C.
1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERTHY SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 953.8; DB 1;
Pred. No. 1.9e-275;
0; Mismatches 2;
                                                                                                                                GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: TRASAKI, AKIO
APPLICANT: STORA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80-074-0 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY AGENT INFORMATION:
NAME: Oblon, No. 5591633man F.
REGISTATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
FILING DATE: 20-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
                                                                                                         Sequence 4, Application US/08125746
Patent No. 5591633
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TELEFAX: (703) 413-3200
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                               ADDRESSEE: P.C. STREET: 1755 S. CITY: Arlington STATE: Virginla COUNTRY: U.S.A. ZIP: 22202
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955; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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Best Local S:
Matches 955
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                                                                                                                                             209 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG
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                                          ATGGCACAGGTTCTCAGAGGCACTGTGACTGCCTTCCCTGGATTTGATGAGCGGGCTGAT
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APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chattenya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 31.7%; Score 311; DB 4; L
Best Local Similarity 99.4%; Pred. No. 2.1e-83;
Matches 311; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Sequence 261, Application US/09542615A
; Patent No. 6518256
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LCCATION: (1)...(401)

CTHER INFORMATION: n = A,T,C or G

US-09-542-615A-261
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389 AAGGGAGCTGGAA 401
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LENGTH: 401
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                                                                                                                                                                                                                                                                                                                                                                                    ch 31.7%; Score 311; DB 4; Length 401; Il Similarity 99.4%; Pred. No. 2.1e-83; 311; Conservative 0; Mismatches 2; Indels
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Fatent No. 6483597

GENERAL INFORMATION

APPLICANT: Wang, Tongtong

APPLICANT: Hosken, Nancy A.

APPLICANT: Hosken, Nancy A.

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

TITLE OF 
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 261
LENGTH: 401
                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LCCATION: (1)...(401)
CTHER INFORMATION: n = A,T,C or G
US-09-643-597-261
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; OTHER INFORMATION: n = A,T,C or
US-09-480-884A-261
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LOCATION: (1)...(401)
                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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Best Local S
Matches 311
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                                                                                                                                                                                                                      APPLICANT: Rails, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Kanger, Aljun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C99
CUBRENT APPLICATION NUMBER: US/09/606,421B
CUBRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOCTUMARE: FastSEQ for Mindows Version 3.0
SEQ ID NO 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 401
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99.4%; Pred. No. 2.1e-83;
tive 0; Mismatches 2.
                                                                                                                                                    Sequence 261, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; LOCATION: (1)...(401)
; OTHER INFORMATION: n = A,T,C or G
US-09-606-421B-261
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US-08-526-136-1
; Sequence 1, Application US/08526136
                                                                     11111111111111111389 AAGGGAGCTGGAA 401
                                                        AAGGGAGCTGGAA 334
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Matches 311; Conservative
                                                                                                                                                                                              APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                       US-09-606-421B-261
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                                                                                                                                                                                     ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFFWARE: WordPerfect (Version 5.0)
CURRET APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 310.8; DB 3;
Pred. No. 5.6e-83;
0; Mismatches 397;
                       et al
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
GENERAL INFORMATION:
APPLICANT: TOWLE, Christine A.
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                              ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.7%;
58.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-526-136-1
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                                                                                                                                  CITY: Boston
STATE: Massach
COUNTRY: U.S.A
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Best Local Simil
Matches 549; (
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TOPOLOGY: linear
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1025 GAACAGAGTCTACAAGACCAGAAAAGACCCTGGAGGAGGCCATTCGGAGGACCAC 1084
                                                                 .205 CCGCCTGGGAACAGATGAGTTCAATGCGATTCTGTGCTCCCGGAGCCGGCCCA 1264
                                                                                                                                                                                                                                                                                                       515
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                                                                                                                                                                                                                                                                             696 TGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTTGTGAAATCTATTCG 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGGAGTTTAGGAAGAATTTTGCCACCTCTTTATTCCATGATTAAGGGAGATACATC 935
                                                                                                                                                                                                                                    516 TGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACT
                                                                                                                                  1145 AAACGTGGACATGACCCTTGTCCAGAGATGTGCAGGAGCTCTATGCAGCTGGGGAGAA
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                                                 TTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAACAGAGACCCTGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDLIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: MOSTOPERCECT (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTONNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TOALS, Christine A. et TITLE OF INVENTION: ANNEXIN XI NUMBER OF SEQUENCES: 36 CARESPONDENCE ADDRESS: ADDRESSE: Fish 6 Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Massachusetts
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PRIOR APPLICATION DATA:
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STATE: Massac
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1151 AAACGTGGACATGACCCTTGTCCAGAGAGATGTGCAGGAGCTCTATGCAGCTGGGGAGA 1210
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                                                                                                                                                                                                                                                                                                                                                                   36 CAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGGGGGCTGATGCAGAAACTCTTCG
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                                                                                                                                                                                                                                                                                      Length 2311;
                                                                                                                                                                                                                                                                                      31.7%; Score 310.8; DB 3; 58.0%; Pred. No. 5.6e-83;
                                                                                                                                                                                                                                                                                                      Pred. No. 5.6e-83;
0; Mismatches 397;
REGISTRATION NUMBER: 30,162
REPERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUTCATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                         33
                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        Best Local Similarity 58.0
Matches 549; Conservative
                                                                                                                                                              LENGTH: 2311
TYPE: nucleic acid
STRANDEDNESS: single
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1071 AGCAG------AGAGGAAACATGGTCCCAGTCTTCACCCAGCGAAATCCTGAACAC 1121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        697 GACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTTGTGAAATCTATTCGA 756
                                                                                                    400 CAAGTTTATGAAGAATATGGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCA 459
                                                                                                                                                                                        891 GCAGTCTACAAACACAAATTTCCAGGTGGAGGCTGTGGATGACATCACATCTGAGACCAGT 950
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                                                                                                                                                                                                                                                                                                                    ---ATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACTT
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Patent No. 6262333

GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Rathleen E.
APPLICANT: Bushell, Steven E.
APPLICANT: Bushell, Steven E.
APPLICANT: Cariol, Theodore J.
APPLICANT: Cariol, Theodore J.
APPLICANT: Cation, Theodore J.
APPLICANT: Cation, Theodore J.
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
BARLIER FILING DATE: 1999-06-10
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                 GAAGGAGTTTAGGAAGAATTTTGCCACCTCTTTATTCCATGATTAAGGGAGATACATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 134.6; DB 4;
Pred. No. 2.4e-30;
0; Mismatches 479;
                                                                                                                                                                                                                                            Sequence 747, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 747
LENGTH: 1793
                                                                                                                                                                                                                                                                                    APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Chang, Jie
APPLICANT: Ren, Fellyan
APPLICANT: Ren, Fellyan
APPLICANT: Wehrman, Tom
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Mang, Jinng
APPLICANT: Mang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
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Best Local Similarity 48.0
Matches 454; Conservative
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; LOCATION: (435)..(1472)
US-09-620-312D-747
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ORGANISM: Homo saplens
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burges, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Garroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD.-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                               Score 123.6; DB 3;
Pred. No. 2.9e-27;
0; Mismatches 241;
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 721
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Patent No. 6262333
                                                                                                                           ; LCCATION: (1)...(644)
; OTHER INFORMATION: n = A,T,C or
US-09-328-111-721
                                                                                                                                                                                                 Query Match 12.6%;
Best Local Similarity 52.6%;
Matches 267; Conservative
                                                                                                               NAME/KEY: misc_feature
                                                          TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                            Length 502;
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Best Local Similarity 53.6%; Pred. No. 3e-19;
Matches 201; Conservative 0; Mismatches 174;
                 EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: August 28, 2003, 19:41:17 le : 57.3333 secs
CURRENT FILING DATE: 1999-06-08
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                                                                                                                                                                 ORGANISM: Homo sapiens
US-09-328-111-625
                                                                                                      SEQ ID NO 625
LENGTH: 502
                                                                                                                                                TYPE: DNA
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August 28, 2003, 15:43:40; Search time 216.333 Seconds (without alignments) 12241.057 Million cell updates/sec
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1 atggcatgtggctgcggtca.....tgctctccggagagatgac 981
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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N_Geneseq_19Jun03:*

| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SOMMAKIES	
Result No.	Score	Query Match	Query Autch Length DB ID	DB	ID	Description
-	981	100.0	981	22	AAC91370	Modified human ann
7	976.2	99.5		22	AAC91368	Modified human ann
m	976.2	99.5		22	AAC91369	Modified human ann
4	957.8	97.6	1466	10	AAN91353	Vascular anti-coad
S	956.8	97.5		6		Plasmid contq. pla
9	956.8	97.5		25		Human cDNA #162 di
7	956.8	97.5		10	AAN91821	Endonexin II compl
80	956.2	97.5		10	AAN90112	Anticoaquiant PP4

Annexin V/urokinas PAP-I cDNA from hu		Sequence encoaing Sequence encoaing	Human lipocortin-V	Lung cancer associ	Toxicologically re	Mouse ischaemic co	Rat sequence diffe	Human annexin V pr	Modified annexin p	Human novel polynu	PAP-I-protein C fu	PAP-I-protein C fu	Bovine EST associa	Bovine EST associa	Coding strand of c	Bovine EST associa	cDNA encoding huma	Human cancer assoc	Human cervical can	Human ovarian tumo	Human cDNA #220 di	Human placenta-der	DNA encoding novel	Human cDNA differe	Gene #3844 used to	cDNA of human plac	Human NOVX polynuc	Human colon cancer	Phase-1 Rat CT gen	Human lung cancer-	Human lung cancer	ang	X	Annexin XI gene in
AAN82107	AA012679	AANBUBUI AANBUB73	AAN90599	AAF18269	AB283344	ABI99289	ABK63699	ABZ21925	ABZ21926	ABX05088	AAQ12681	AAQ12680	ABX47939	ABX36749	AAN90772	ABX42696	ABS76372	AAC77826	AAH72826	AAZ77514	ABX63220	AAQ02888	AAS93800	ABK84730	ABN97346	AAQ02887	ABX72249	ABQ59306	ABT09335	AAC65957	ABQ92362	ABL49176		AAQ39150
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97.4	97.4		97.0				74.1		52.8								•	•			•	35.5						32.6	32.1	31.7	31.7	31.7	31.7	31.4
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ALIGNMENTS

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							Modified human annexin nucleotide sequence, SEQ ID NO:		Human; annexin; chelation site; nuclear imaging; apoptosis;																			Nowel modified approain macked for imparing granular thrombi	Vascutat
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	AAC91370 standard; DNA; 981				(first entry)		nnexin		chelati	transplant rejection; ds.								25-MAY-2000; 2000WO-US14324.		99US-0324096.		(UNIW) UNIV WASHINGTON.		DS;		.09		4	ווובאדוו
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chelation site; nuclear imaging; apoptosis;

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Modified human annexin nucleotide sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombl or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin bloactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTGGAAAATTTGAAAAATTAATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCT
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                                                                                                                                                                                                                                                                                                                             Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid extension which comprises a glycine and a cysteine residue -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.5%; Score 976.2; DB 22; Length 99.7%; Pred. No. 3.3e-273; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 981 BP; 286 A; 187 C; 251 G; 257 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 26; Page 31-33; 39pp; English
                                                                                                                              99US-0324096
                                                                                  2000WO-US14324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  il Similarity 99.7
978; Conservative
                                                                                                                                                                          (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                            WPI; 2001-080465/09.
P-PSDB; AAB50864.
                                                                                                                                                                                                                     Tait JF, Brown DS;
WO200073332-A1
                                                                                  25-MAY-2000;
                                                                                                                              01-JUN-1999;
                                         07-DEC-2000
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The vascular anti-coagulating protein (VAC)-alpha encoded by this cDNA is used in the preparation of monoclonal antibodies (WAbs). The VAC-alpha is injected into a host animal, in conjugation with eg keyhole limpet haemocyanin, and the B-cells from the immunised hosts are then fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-alpha. The Abs can be used as immunoassay reagents to detect VAC proteins, as affinity ligands for purificn. of VACs and as medicaments for binding and/or neutralising VAC proteins in (Updated on 10-WAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGGAGCATCCTGAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 TATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGGGGGTGA
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                                                                                                               Monoclonal antibodies to vascular anti-coagulating proteins hybridomas producing such antibodies.
                                                                                                                                                                                                                                                                                                           Sequence 1466 BP; 423 A; 291 C; 327 G; 425 T; 0 other;
                                                                                                                                                 Disclosure; flg 1; 11pp; German
                                 (BOEH ) BOEHRINGER INGELHEIM.
          88DE-3810331
                                                                              WPI: 1989-293724/41
                                                                                        P-PSDB; AAP91953
          26-MAR-1988;
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         ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATAT
                      GGCTCAAGCCTGGAAGATGACGTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTG
                                                                                                                                                CAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG
                                                                                                                                                                                                                                                                                                                                                                               proteins; hybridomas; B-cells; myelomas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vascular anti-coagulating protein-alpha cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                  cription terminator in addition to the placental coagulation inhibitor gene. The polypeptide produced on culturing of transformed host cells exhibits strong anticoagulant activities and is useful for the treatment and prevention of eg thrombosis or disseminated intravascular coagulation in the brain, heart and peripheral blood vessels. (Updated on 10-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT
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                                                                                                                                                                                                                                                                                                                                                    Score 956.8; DB 9;
Pred. No. 1.8e-267;
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                                                                                                                                                                                                                                                                                                              Sequence 1567 BP; 430 A; 332 C; 358 G; 447 T; 0
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99.8%;
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958; Conservative
                                                                   recombinant DNA
                             Page
                             Disclosure;
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AATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGT
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This invention relates to a combination comprising several CDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially carpeased cDNAs in a sample. The cDNAs of the invention may have antiaterlosclerotic; cytostatic; cardiant; hypotensive; antidiabetic; gynaecological; vasctropic and cerebroprotective activities and may be used in gene therapy. The cDNAs of the invention may be used in a high-throughput methods for detecting differential expression of one or neer cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a nation that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify an antural or recombinant protein from a sample. The uncleotides may be useful for diagnosing, staging, treating, or monitoring the progression of a vascular disease, e.g. atherosclerosis, cancer, coronary artery disease, hypertension, diabetes, pre-clampsia, ischaemia creperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new
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cardiant; hypotensive; antidiabetic; gynaecological; vasotropic;
cerebroprotective; gene therapy; vascular disease; cancer; coronary;
attery disease; hypertension; diabetes; pre-eclampsia; restenosis;
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                                                                          Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at http.seqdata.uspto.gov/sequence.html?DocID=20020137081.
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            cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, amount or distribution of the protein. The present sequence represents a cDNA of the invention that is differentially expressed in
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                                                                                                                                                                       CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA
                                                                                                                                                                                                                                                     CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATT
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                                                                          GAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC
                                                                                                                   GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC
                                                                                                                                                            AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
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/*tag= a
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(first entry)
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22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGGAGCATCCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 1605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hENII is a calcium and phospholipid binding protein (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.5%; Score 956.8; DB 10.
99.8%; Pred. No. 1.8e-267;
1ve 0; Mismatches 2;
                                                                                                                                                                                                                                         Location/Qualifiers
160..1119
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                   (RORE ) RORER INT OVERSEAS INC
                                                                                                     AAN91821 standard; DNA; 1605
                                                                                                                                                                                                                                                                                                                                               88US-0176802.
                                                                                                                                                                                                                                                                                                                           89EP-0105626
                                                                                                                                                                                                 Placenta; blood coagulation
                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                           Endonexin II complete cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 99.8
les 958; Conservative
                                                                                                                                                                                                                       Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1989-317181/44.
P-PSDB; AAP91021.
                                                                                                                                                                                                                                                                                                                                                                                         Jaye M;
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16-MAR-1990
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946 TCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTTTTTTCCATGAT 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             carrier; thrombus; thrombolytic; fusion protein; fibrinolysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as a carrier molecule to build a thrombus-targeting thrombolytic fusion protein. The protein is the result of expression of a fusion gene (this sequence) comprising the Annexin V gene and a low-molecular urokinase gene, in insect cells, the Annexin V-scu-PA-32 fusion protein, expressed in insect cells train Tn-5B1-4, has high affinity for active
                                                                                                      TGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGAA
                                                                 TCTGTTTAACATCAGGAAGGACTTTAGGAAGAATTTGCCACCTCTCTTATTCCATGAT
                                                                                                                                                                                                           921 TAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGA
 681 AATTGAGGAAACCATTGACGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGT
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1..1803
/*tag= a //
/product= "annexin V/urokinase fusion protein"
/note= "no start or stop codons are given at the or 3' ends of the sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annexin V, which has high affinity for active thrombocytes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 •
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New thrombolytic fusion protein for targetting thrombus fusion of Annexin V and urokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Annexin V/urokinase fusion construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Page 2-4; 20pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                      AAA11241 standard; DNA; 1803 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99CN-0113524.
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                                                                                                                              New DNA sequence encoding anticoagulant PP4 protein - and new recombinant protein, vectors, antibodies, etc., useful therapeutically and diagnostically.
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                   Sequence 1575 BP; 461 A; 322 C; 351 G; 441 T; 0 other;
                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                        DNA sequence encoding anticoagulant PP4 protein. inhibits blood coagulation at the thromboplastin. The derived protein is 320 amino acids. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                        .;
                                                                                                                                                                                                                                                                                                                           97.5%; Score 956.2; DB 10 99.7%; Pred. No. 2.7e-267 cive 0; Mismatches 3
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                                                                              Kupper
                                                                                                                                                                                Claim 1; table 1; 14pp; German.
 88EP-0118039
                         87DE-3737239
                                                                                                                                                                                                                                                                                                                                         al Similarity 99.7
958; Conservative
                                                   (BEHW ) BEHRINGWERKE AG.
                                                                             Abel KJ,
                                                                                                      WPI; 1989-166767/23.
                                                                             Grundmann U,
29-OCT-1988;
                         03-NOV-1987;
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142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201
                                                                                                                                                                                     PAP-I; anticoagulant; anti-inflammatory agent; phospholipid; phospholipase A2; disseminated intravacular coagulation; human placenta; deep vein thrombosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human proteins having anticoagulant and antiinflammatory activity - isolated from biological fluid by anion-exchange chromatographoc media
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 ATGCCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGGGGGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A human placenta cDNA library (Clontech) was screened to obtain this sequence. The cDNA does not contain a leader peptide sequence, indicating that PAP-I is probably not constitutively secreted. The product binds to phospholipid and inhibits phopholipase A2. The protein can substitute heparin or other anticoagulants in the treatment of disseminated intravascular coagulation, deep vein thrombosis, or other disorders. It also has antiinflammatory
                                                                                                                                                               PAP-1 cDNA from human placenta, used for anticoagulant production
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                                                 DB 21; Length 1803,
thrombocytes and has the fibrinolytic activity of urokinase
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                        Sequence 1803 BP; 495 A; 415 C; 462 G; 431 T; 0 other;
                                               Score 955.6; DB 21
Pred. No. 4.3e-267;
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Best Local Similarity 99.6%;
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ATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG
                                           GAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC
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                Phopholipid; binding protein; lipocortin; domain; vitamin K;
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Pred. No. 5.1e-267;
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                                                                                                                              Sequence encoding vascular anticoagulating protein (VAP) VAC-alpha
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                                                                                                     and highly purified VAPS, constructing DNA probes on the basis of this sequence, using the probes to search through suitable CDNA libraries, isolating cDNA that hypridises with the probes. by inserting the CDNA into a suitable vector, and using the vector to transform a host organism. VAC-alpha has anticoagulant activity under certain conditions, but loses this activity in the event of severe bleeding. It acts by inhibiting conversion of factor X to factor Xa and conversion of prothrombin to thrombin. It is structurally related to lipocortin in has similar antihiflammatory and phospholipase inhibitory activity. (Updated on 25-MAR-2003 to correct PR field.)
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Pred. No. 7.6e-267;
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vascular anti:coagulating proteins
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                                         Falkner
AATTCAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGT
             TCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTTTTATTCCATGAT
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Reutlingsperger
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organism. VAC-alpha has anticoagulant activity under certain conditions, but loses this activity in the event of severe bleeding. It acts by inhibiting conversion of factor X to factor Xs and conversion of prothrombin to thrombin. It is structurally related to lipocortin (Nature, 320, 77, 1986) and lipocortin II (Cell, 46, 191/120, 1986) and has similar antilinflammatory and phospholipase inhibitory activity. (Updated on 25-WAR-2003 to correct PR field.)
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CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA
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                                                                                                                                                                    Human lipocortin-V; lambdaRLipo V-1; anti-inflammatory agent.
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Pred. No. 4.5e-266;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            See also AAP91362, AAN90598, and AAP91363.
                                                                                                                                                                                                                                                                                                                                                    Browning JL;
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/*tag= a
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                                                                                     AAN90599 standard; cDNA; 1574
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Best Local Similarity 99.5%;
Matches 955; Conservative
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                                                                                                                                                                                                                                                                                                                                                  Pepinsky RB,
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P-PSDB; AAP91363.
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773 CGAAGIGI-NCTCATITGAGAAAGGIGITIGACAAGIACAIGACIATATCAGGATITICAA

682 ATTGAGGAAACCATTGACCGGGGGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT

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CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA

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561 712 621 772 681 831 741 891

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polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58540. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; and antagonists may have neuroprotective; cytostatic; cardioactive; cardioactive; cardioactive; cardioactive; dimmunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; ginecological; or antibacterial activity. The invention also includes antibodies specific for the activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other disorders such as neural; immune, muscular, reproductive, castactive gastrointestinal, pulmonary, cardiovascular, reproductive, disorders such as neural; and proteins may also be used in the treatment of wounds and thectious diseases. Polynucleotide sequences AAF18435 and peptide AAB58549 are used in the course of the invention for the activitication and characterisation of the polynucleotide and protein
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                                                                                                                                                                                                                                   Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer -
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Pred. No. 1.1e-263;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                   Claim 1; Page 746; 1425pp; English.
                                                                            (HUMA-) HUMAN GENOME SCI INC. (ROSE/) ROSEN C A.
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  08-MAR-2000; 2000WO-US05918.
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956; Conservative
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P-PSDB; AAB58393.
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473 382 533 442

GAACTGAGAGCCATCAAACAAGTTTATGAAGAATATGGCTCAAGCCTGGAAGATGAC

GTGGTGGGGGACACTTCAGGGTACTACCAGGGATGTTGGTGGTTCTCCTTCAGGCTAAC 501

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742 GIGAAAICIAIICGAAGIAIACCIGCCIACCIIGCAGAGACCCICIAITAIGCIAIGAAG 801

| GGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTTCCAGGAGTGAGATTGAT

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GenCore version 5.1.6
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	August 28, 2003, 15:43:40; Search time 2602.33 Seconds (without alignments) 15421.677 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-970-969-5 981 1 atggcatgtggctgcggtcatgctctccggagagatgac 981
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 seqs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
Database : GenEmbl:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Qy 961 CTGCTCTCGGAGAAGATGAC 981 · 	RESULT 2 AR26469 LOCUS LOCUS LOCUS DEFINITION Sequence 1 from patent US 6323313. ACCESSION AR262469.1 GI:28073913 KEYWORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. TITLE ADTHURS Tait,J.F. and Brown,D.S. TITLE ADTHURS Tait,J.F. and Brown,D.S. TITLE ADTHURS SOURCE LOCATION/Qualifiers JOURNAL PATENTIAL JOURNAL LOCATION/Qualifiers SOURCE 1.981 AUTHUR JOURNAL JOURNAL JOURNAL JOURNAL JOURNAL ACCESSION JOURNAL JO	Query Match 99.5%; Score 976.2; DB 6; Length 981; Best Local Similarity 99.7%; Pred. No. 8.1e-247; Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 ATGGCATGTGGCTGCGGTCATATGGCAGGTTCTCAGAGGCACTGTGACTTCCCT 60 Db 1 ATGCATGTGGCGGTGCCATATGGCAAGTTCTCAGAGGCACTTTGACTTCCCT 60	QY 61 GGATTTGATGAGGGGCTGATGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120	121 GATGAGGAGAGCATCCTGACTCTGACATCCCGAAGTAATGCTCAGCGCAGGAAATC 181 TCTGCAGCTTTTAAGACTCTGTTTGGCAGGGATCTTCTGGATGACCTGAAATCAATATCTTTAAGACTCTGTTTGGCAGGGATCTTCTGGATGACCTGAAATCAAATCAAATCAAATCAAATCAAATCAAAATCAAAATCAAAATCAAAATCAAAATCAGATGACCTGAAATCAGAAACTAAAATCAGGAACTTTTAAAAACTCTGTTTGGCAGGAATCTTCTGGATGACCTGAAATCAGAAACTAAAATCAGAACTAAAATCAGAAACTAAAATCAGAAACTAAAAATCAGAAACTAAAAAAAA	OY 241 ACTGGAAAATTGAAAATTGGCCCTGGTGAACCCTCTGGCCTTTATGATCT 300	QY 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAATAT 420 Db 1	481 GTGGTTCTCCTTCAGGCTAACAGAGCCCTGATGGAATTGATGAAGCTCAAGTTGAA 481 GTGGTTCTCCTTCAGGCTAACAGAGCCCTGATGGAATTGATGAAGCTCAAGTTGAA 481 GTGGTTCTCCTTCAGGCTAACAGAGCCCTGATGGAATTGATGAAGAGCTCAAGTTGAA	Oy 541 CAAGNIGCTAAGTTATTCAGGTGGAGAACTTAATGGGGGACAGATGAAGAAAG 600
source 1981 /organism="unknown" BASE COUNT 286 a 187 c 250 g 258 t	Query Match 100.0%; Score 981; DB 6; Length 981; Best Local Similarity 100.0%; Pred. No. 4.4e-248; 0; Indels 0; Matches 981; Conservative 0; Mismatches 0; Indels 0; 1 ArGGCARGTGGGGGGCAGATAGGGAAGGTTCTCAGAGGCACTGGACTGCACTTCCCT 0 111111111111111111111111111111111111	241 ACTGGAAAATTGAAAAATTAATTGGCCTCTGGATGAACCCTCTCGGCTTTATGATGCT 300 11111111111111111111111111111111111	361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAAGATAT 420 		541 CAAGATGCTCAGGCTTTATTTCAGGCTGGACAACTTAAATGGGGGACAGATGAAGAAAG 600 [1]1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	661 ATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTA 720	ACCTCTATTATCCTATGAAGGAGCTGGGACAGATGATCATACCTCATCATGAGAGAGA	841 GTTTCCAGAGTGAATTGATTTAACATCAGGAGGATTAGGAAGAATTTTGCC 900 841 GTTTCCAGGAGTGATTGATTTAACATCAGGAGGATTTAGGAAGAATTTTGCC 900 841 GTTTCCAGGAGTGATTGATCTGTTTAACATCAGGAGGATTTAGGAAGAATTTTGCC 900 901 ACCTCTTTATTCCATGATTAAGGAGAATACATCTGGGGACTATAAGAAAGCTCTTCTG 960 11111111111111111111111111111111111

0y 361 ATTGCTTCAAGGACACCTGAAGACTGAGAGCATCAAAGTTTATGAAGAATAT 420 11111111111111111111111111111111111	481 GTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Qy 601 TTTATCACCATCTTTGGAACACGAAGTGTGTCATTTGAGAAAGGTGTTTGACAAGTAC 660	Qy 721 GAGCAACTACTCCTTGTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAG 780 11111111111111111111111111111111111		RESULT 4 A07367 LOCUS DEFINITION M.musculus VAC-alpha CDNA. ACCESSION A07367 A07367 A07367 ACCESSION A07367 ACCESSION A07367 ACCESSION A07367 ACCESSION A07367 ACCESSION A07367 ACCESSION A07367 AND MUSCULUS (house mouse) REFYNORS SOURCE ORGANISM Mus musculus (house mouse) AND MUSCULUS BUT AND MUSCULUS AND AUTHORS JOURNAL LOCATION/QUALIFIERS JOURNAL AD ARTEF "AND MUSCULUS" AND LAFFE "ARA ADD A" AD ARTEF "ALA ADD AND MUSCULUS" AD ARTEF "AND AND AND AND AND AND AND AND AND AND
Qy 661 ATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACGGGGACTTCTGGCAATTTA 720 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	781 ACCTCTATTATGCTATGGAGGGAGTGGAGTGATGATGTTTTTTTT	QY 901 ACCTCTTTATTCCATGATTAAGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTG 960 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 3 AR262470 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS AR262470 BETHINTION Sequence 3 from patent US 6323313. ACCESSION AR262470.1 GI:28073914 VERSION VERSION VERSION AR262470.1 GI:28073914 VERYORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. AUTHORS Talt.J.F. and Brown.D.S.	TITLE Annexin derivative with endogenous chelation sites JOURNAL Patent: US 6223313-A 3 27-NOV-2001; FEATURES Location/Qualifiers source 1. 981 Aorganism-"unknown" BASE COUNT 286 a 187 c 251 g 257 t	Query Match 99.5%; Score 976.2; DB 6; Length 981; Best Local Similarity 99.7%; Pred. No. 8.1e-247; Indels 978; O. Gaps 0; Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0; QY 1 ArGGANGTGGCTGGCTCATATGGCAGGTTCTCAGAGGCATGTCACTCCCT 60 Indels 0; Gattlill

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Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 9 Row: 1 Column: 8 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4809273. Location/Qualifiers
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VOLETIDIRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSR
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                                                                Length 1466;
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                                                              Score 957.8; DB 6;
Pred. No. 5.9e-242;
0; Mismatches 2;
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Enkaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

Strausberg, N.L.; Feingold, E.A., Grouse, L.H., Derge, J.G.,
Ribusner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.J., Wang, J., Haleh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Torghilyuki, S.,
Carninci, P., Prange, C., Rahe, S.S., Loquellano, N.A., Peters, G.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Youchman, J. W., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butkson, M.C., Rodriguez, A.C., Grimwood, J., Schunutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinsk, M. Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
32388253
1536 bp mRNA linear PRI 06-JUN-2003 annexin A5, mRNA (cDNA clone MGC:4402 IMAGE:2906015),
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Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: MGC help desk

Contact: MGC help desk

Email: cgapbs-rémail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

BC Cancer Agency, Vancouver, BC, Canada

Info@bcgsc.bc.ca
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 1539)

Strausbarg, R.L., Feingold, E.A., Grouse, L., Berge, J.G.

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haleh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Morlay, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Racky, K.C., Hale, S., Garcia, A.M., Gay, L.J., Lu, X., Gibbs, R.A.,

Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Rzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J. E., Jones, S.J. and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BC012804 1539 bp mRNA linear PRI 06-JUN-2003
Homo sapiens annexin A5, mRNA (cDNA clone MGC:2795 IMAGE:2961097),
complete cds.
BC012804 GI:15215411
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                                                                                                                                            GGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA
                                                              AATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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Strausberg, R.
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AUTHORS
TITLE
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VERSION
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AUTHORS
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SEIDLFNIRKEFRRNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
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           /organism="Homo sapiens"
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llarity 99.8%; Pred. No. 5.9e-242;
Conservative 0; Mismatches 2;
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                                                                                                                          /note="Vector: pOTB7"
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Homo sapiens annexin A5, mRNA (cDNA clone MGC:4465 IMAGE:2961097),
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    CGTGGTGGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAA
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Location/Qualifiers
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RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKG
AGTNEKVLTEIIASRRPEELRAIKOVYEEFYGSSLDDVVGOTSGYYGMLVVLLQAN
RDPDAGIDEAQVEQDAQALFYGAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISG
FQIEFTIDRFTSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMYSR
SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="MGC:2795 IMAGE:2961097"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DHIOB-R"
/note="Vector: pOTB7"
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99.8%; Pred. No. 5.9e-242;
Mismatches 25;
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/db_xref="LocusID:308"
/db_xref="MIM:131230"
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/protein_id="AAH12804.1"
/db_xref="G1:15215412"
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Catarrhini; Hominidae; Homo.
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                                    GAAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGA
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1 (bases 1 to 1582)
Grundmann, U., Abel, K.J., Bohn, H., Lobermann, H., Lottspeich, F.
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'RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKFPSRLYDAYELKHALKG
'RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKFPSRLYDAYELKHALKG
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FQIEFTIDRETSGSNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSR
SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD"

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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDM sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                           Direct Submission
Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGGCTGA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/db_ref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 10 Row: k Column: 21. Location/Qualifiers
1. 1539
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Pred. No. 5.9e-242;
); Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //octe="synonyms: ANX5,
/db_xref="LocusID:308"
/db_xref="MIM:131230"
                                                                                                                                                                                                                                          Contact: MGC help desk
Email: cgapbs-rêmail.nih.gov
Tissue Procurement: ATCC
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al Similarity 99.8%;
959; Conservative
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1. .963
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FOIEFIIDRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVWVSR
SEIDLENIRKEFRKRFATSLYSMIKGGTSGDYKKALLLLCGEDD"
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DNA sequence (gaa) for vascular anticoagulating protein.
A01769 GI:410787
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Pred. No. 1.1e-241;
0; Mismatches 2;
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Patent: WO 8807576-A 1 06-OCT-1988;
Location/Qualifiers
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ilarity 99.8%;
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PODAGIDEAQVEQDAQALEYGAGELRAKATDEERETTITGTSTSYSHLRKYFDKYMTISG
FQIEETIDRETSGHLAAVKSIRSIPAYLAETIYYAMKGAGTDDHTLIRVMVSR
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                                                                                                                                                                                                                                                                                                                                                                   /translation="MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTS
RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKG
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   Characterization of cDNA encoding human placental anticoagulant
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                                                                                                                                                                                                                                                                                                                   /product="anticoagulant protein 4"
/protein_id="AAB59545.1"
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                                                                                                                                                                      /organism="Homo sapiens"
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<1. 1582
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/codon_start=1
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02-DEC-1994

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1432 bp Sequence 21 from Patent EP 0330396. 107345 107345.1 GI:590053

RESULT 10 107345 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

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Fujikawa,K., Irani,M.H. and Carter,B.L.A.
HUMAN PROPEINS HAVING ANTICOAGULANT AND ANTI-INFLAMMATORY ACTIVITY
Patent: WO 8005659-A 3 11-AUG-1988;
Location/Qualifiers
1. .1454
                                                                                               AAGGGAGCTGGAACAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA
                                                                                                                                              CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATT
                                                                                    GAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC
                                                                                                                                  GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC
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Pred. No. 1.1e-241;
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M18366.1 GI:179131
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RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKG
AGTNEKVLTEIIASRRPBELAAIKOYYEEFYGSEDDVYGDTSGYYORMLVYLLQAN
RDPDAGIDEOTSGYYODAQALEKWGTDEEKFITIFGTRSVSHLKVFDKYMTISG
FQIEDTIDRETSGHLAQLLLAVYSIRSIPAYLAETLIYAMKGAGTDDHTLIRVMYSR
SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD*
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Homo saplens (human)

Homo saplens

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota, Metazoa, Chordata; Catarrhin; Hominidae; Homo.

| (bases 1 to 1444)

| (bases 1 to 1444)

| Primary structure of human placental anticoagulant protein

Blochemistry 26 (25), 8087-8092 (1987)
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Location/Qualifiers
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Pred. No. 1.1e-241;
0; Mismatches 2;
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/note="anticoagulant precursor
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/db_xref="GI:179132"
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/product="ATC mRNA"
13. .975</pre>
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/product-"annexin A5"
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/protein_id-"AAB01429_1"
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RDPDAGIDEAQVEGDAAALFQAGELKWGTDEEKFTITFGTRSVSHLRKVFDYYMTISG
FQIEFTIDREFSGALAAVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSR
SEIDLENIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
                                                                                                                                                                                                                                                                                   Contact:
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,O.L., Maslello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: o Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 219480.
Location/Qualifiers
                 Euteleostomí;
                                                                      Direct Submission
Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/TIP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Strausberg, R.
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//tissue_rype="Ovary, adenocarcinoma"
//clone_lib="NIH_MGC_9"
/lab_host="DH108-R"
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Pred. No. 1.1e-241;
); Mismatches 2;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="LocusID:308"
/db_xref="taxon:9606"
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/protedin_id="CAA30985.1"
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RDPDAGIDEAQVEQDAAALFGAGELKWGTDEEKFTITFGTRSVSHYRKYFDKYTISG
FQIEFTIDRFFSGULLAVVKSIRSIPAYLAFTITFGTRSVSHYRWTISG
SEIDLFNIRKEFFRKNFATSLYSMIKGDTSGDYKRALLLLCGEDD"
                                           Direct Submission
Submitted (15-AUG-1988) Hauptmann R., Ernst Boehringer Institut
fuer Arzneimittelforschung, Dr. Boehringer-Gasse 5/11, A-1121 Wien,
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1. 1560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="lambda pl1/3 and others"
/tissue_type="placental"
124. 133
/note="Rozak consensus (tcgccatgg)"
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/note="structural repeat (67 AA)"
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/note="VAC protein (AA 1-320)"
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/note="structural repeat (67
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/note="structural repeat (67
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1560)
Maurer-Fogy,I., Reutelingsperger,C.P., Pieters,J., Bodo,G.,
Stratowa,C. and Hauptmann,R.
Cloning and expression of cDNA for human vascular anticoagulant,
Ca2+-dependent phospholipid-binding protein
Bur. J. Biochem. 174 (4), 585-592 (1988)
                          AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA
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Pred. No. 1.1e-241;
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  /product-'human
                    /product*'human
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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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C12P21/02,C07K13/00,C12N15/00//A61K37/02,(C12P21/02,C12R1:19);
strandedness: Double;
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1 (Dases 1 to 1566)
Saino,S., Iwasaki,A. and Suda,M.
POLYPEPTIDE HAVING ANTI-BLOOD COGULATING ACTION
PAtent: JP 1989020095-A 1 24-JAN-1989;
KOWA CO
                                                                                                                                                 GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC
                                                                    AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
                                                                              CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA
                                                                                                                     GGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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clone=pMKT7;
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136. .1098
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20-FEB-1987 JP 87P 372:
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JP 1989020095-A/1
24-JAN-1989
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hypothetical: No;
anti-sense: No;
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JP 1989020095-A/1.
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Homo sapiens
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976 da		103
Qy 922	922 AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAGATGAC 981	981
Db 1036	1036 AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTGGAGAAGATGAC 1095	1095
Search completed: August Job time : 2604.33 secs	Search completed: August 28, 2003, 18:14:05 Job time : 2604.33 secs	

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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August 28, 2003, 15:43:40; Search time 2602.33 Seconds (without alignments) 15421.677 Million cell updates/sec US-09-970-969-3 981 1 atggcaggtggctgtggcca......tgctctccggagaagatgac 981 OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Run on:

2888711 seqs, 20454813386 residues Searched:

5777422 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

9b_ba:*
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Pred. No. is the number of results predicted by chance to have a

em_htgo_mus: * em_htgo_other: * em_htgo_hum:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	62470 Seq 62469 Seq 62469 Seq 62471 Seq 64271 Homes 112804 Homes 12802 Homes 1345 Seques 1365 Human 1375 Seques 1375 Seques 1372 Homes 1372 Homes 1372 Homes 1372 Homes 1373 Human 1383 Seques 1383 Seques 1384 Human 1384 Human 1384 Human 1384 Seques 1410 Seques 1411 Seque	DNA linear PAT 29-JAN-2003
SUMMARIES .h DB ID	6 AR26247 6 AR26247 6 AR262467 9 BC012809 9 BC012809 9 BC012809 9 HUMPAPA 6 E01816 6 E01817 6 E01817 6 E01817 6 E01818 6 E01818 6 A0174 9 BC01867 10 AK01037 10 AK01037 10 AK01037 10 AK01037 10 AK01037 10 AK01037 10 AK01037 10 AK01037 10 AK01037 10 AK01037 11 AK01033 12 A0177 13 A0177 14 BCOKNUEX	981 bp 28073914 28073914 981) 11ve with endogenous 3113-A 3 27-NOV-2001; on/Qualifiers
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Result No.	102 4 2 3 4 7 9 6 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 AR262470 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JORNAL FEATURES

Oy 961 CTGCTCTCGGAGAGATGAC 981 	RESULT 2 AR262469 LOCUS DEFINITION Sequence 1 from patent US 6323313. ACCESSION Sequence 1 from patent US 6323313. ACCESSION AR26469.1 GI:28073913 KEYWORDS SOURCE Unclassified. Unclassified. Inclassified. Talt.J.F. and Brown, D.S. TITLE AUTHORS Talt.J.F. and Brown, D.S. TITLE Annexin derivative with endogenous chelation sites JOURNAL Patent: US 6323313-A 127-NOV-2001; FEATURES I. 981 Authors JOURNAL Patent: US 6323313-A 127-NOV-2001; FEATURES I. 981 Authors JOURNAL Patent: US 6323313-A 127-NOV-2001; FEATURES II. 981 Authors JOURNAL PATENT INCLASSION STATES JOURNAL PATENT STATES JOURNAL P	Query Match 99.7%; Score 977.8; DB 6; Length 981; Best Local Similarity 99.8%; Pred. No. 2.4e-247; Matches 979; Conservative 0; Mismatches 2; Indels 0; Gaps 1 ATGGCAGGTGGCCATATGGCACATCTCAGAGGCACTGTGACTTCCCT 1 11111	OY 61 GGATTTGATGAGCGGCTGATGCACAAACTCTTCGGAAGGCTATGAAAGGCTTGGCACA 120 Db 61 GGATTTGATGAGCGGCCTGATGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120 61 GGATTTGATGAGCGGCCTGATGCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACA 120	OY 121 GATGAGGAGCATCCTGACTCTGTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATC 180 121 GATGAGGAGAGCATCCTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATC 180	OY 181 TCTGCAGCTTTAAGACTCTGTTTGGCAGGGATCTTCTGGATGACTGAAATCAGAACTA 240	OY 241 ACTGGAAAATTGAAAAATTGTGGCTCTGAAGAACCCTCTGGCTTATGATGCT 300 11111111111111111111111111111111111	OY 301 TATGAACTGAAACATGCCTTGAAGGGGGGCTGGAACAAATGAAAAGTACTGACAGAAATT 360 	OY 361 ATTGCTTCAAGGACACCTGAAGAACTGAGAGCCATCAAACAAGTTTATGAAGAAATAT 420 	OY 421 GGCTCAAGCCTGGAAGATGACGTGGGGGACACTTCAGGGTACTACCAGGGATGTTG 480	OY 481 GTGGTTCTCCTTCAGGGTAACAGAGACCCTGATGTGGAATTGATGAAGGTCAAGTTGAA 540	QY 541 CAAGATGCTCAGGCTTTATTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAG 600 	Oy 601 TTFATCACCATCTTTGGAACACGAAGTGTCTCATTTGAGAAAGGTGTTTGACAAGTAC 660
source 1981 /organism="unknown" /organism="unknown" /orgin	Query Match 100.0%; Score 981; DB 6; Length 981; Best Local Similarity 100.0%; Pred. No. 3.4e-248; 0; Gaps 0; Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 ArGGCAGGTGGGCATATGCAAAGTTCTCAGAGCACTGTGACTGAC	241 ACTGGAAAATTTGAAAATTAATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCT 300		421 GGCTCAAGCCTGGAAGATGACGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTG 480 	481 GTGGTTCTCCTTCAGGCTAACAGAGCCCTGATGCTGGAATTGATGATGAGGTCAAGTTGA 540 	541 CAAGATGCTCAGGCTTTATTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAG 600 	601 TTTATCACCATCTTTGGAACACGAAGTGTCTCATTTGAGAAGGTGTTTGACAAGTAC 660 	661 ATGACTATATCAGGATTCAAATTGAGGAAACCATTGACGGGAGACTTCTGGCAATTTA 720 	721 GAGCAACTACTCCTTGCTGTTGTAATCTATTCGAAGTATACCTGCCTACCTTGCAGAG 780 	781 ACCCTCTATTATGCTATGAAGGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATG 840 	841 GTTTCCAGGAGTGAGATTGATGTTFAACATCAGGAAGGAGTTFAGGAAGAATTTGCC 900 	901 ACCTCTTTATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTG 960

10	RESULT 4 A07367 LOCUS DETINITION M.musculus VAC-alpha cDNA. A07367.1 G1:412270 KEYWORDS SOURCE Mus musculus REFERENCE Locus ORGANISM Mammalia: Eutheria: Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria: Rodentia; Sciurognathi; Murinae; Mus. REFERENCE Location/Qualiflers JOURNAL FEATURES Location/Qualiflers Loca
09 661 ATCACTATATCACACATTCAAATTCAGGAAACCATTGACCGGGACTTCTGCCAATTTA 720	Query Match 99.54; Score 976.2; DB 6; Length 981; Best Local Similarity 99.74; Pred. No. 6.3e-247; Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0; QY 1 ATGGCAGTGGCCATATGGCACAGGTTCTCAGAGGCACTGGACTGCCT 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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BC004993
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                   Homo saplens
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FQIBETIDRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKQAGTDDHTLIRVMVSR
SEIDLEVIRKEFRKRETSGNLKGDTSGDYRKALLLLCGEDD*
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                                             97.7%; Score 958; DB 6; I
99.5%; Pred. No. 4.1e-242;
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Altschul, S. F., Reaberg, B. Grouse, L. H., Derge, J. G.,
Altschul, S. F., Zeeberg, B., Buttow, K. H., Schaefer, C. W., Bhat, N. K.,
Altschul, S. F., Zeeberg, B., Buttow, K. H., Schaefer, C. F., Bhat, N. K.,
Altschul, S. F., Jordan, H., Moore, T., Max, S. L., Wang, J., Haich, F.,
Diatchenko, L., Maruslana, K., Farmer, A.A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshlyuki, S.,
Carninol, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Morley, K. C., Hale, S., Guaratue, P. H., Richards, S. W.,
Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y.,
Butterfield, Y. S., Krzywinski, M. I., Skalaka, U., Smailus, D. E.,
Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.
Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences
R. 2288257
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Email: cgapba-rémail.nih.gov
Tissue Procurement: ATC/CTD/DTP
Tissue Procurement: ATC/CTD/DTP
CDNA Library Preparation: Rubin Laboratory
Infoêbegsc.bc.ca
Infoêbegsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hsiao, Martin Krzywinski, Refe Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
1536 bp mRNA linear PRI 06-JUN-2003
Homo sapiens annexin A5, mRNA (cDNA clone MGC:4402 IMAGE:2906015),
complete cds.
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Direct Submission
Submitsion
Submitted (21-MAR-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1536)
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administration by Finaless Catalinis; Houselder; House.

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Scheamen, C.M., Bath, R.K.,

Hopkins, R.F., Jordan, H., Morce, T., Max, S.I., Wang, J., Hsieh, F.,

Biatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonnaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Marany, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Kolung, A.C., Shevchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samilus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC012804 1539 bp mRNA linear PRI 06-JUN-2003
Homo sapiens annexin A5, mRNA (cDNA clone MGC:2795 IMAGE:2961097),
complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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               ATGAAGGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAG
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22388257
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Homo sapiens
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Strausberg, R.
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FQIEFTIDREFSGALMALSLYSMIKGTDESKFTIFGTRSVSHLRKVFDYYMTISG
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0; Mismatches 5;
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Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi;
Mammalia; Eutheria: Primates: Catarrhini; Hominidae: Homo.

1. (bases 1 to 1539)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Alischul, S.F., Zeeberg, B., Buetow, K.H., Schaefer C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G. M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Stapleton, M., Malek, J., Bosak, S.A., McEwan, P.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morlay, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Glbbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitling, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC012822 1539 bp mRNA linear PRI 06-JUN-2003
Homo sapiens annexin A5, mRNA (cDNA clone MGC:4465 IMAGE:2961097),
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Series: IRAL Plate: 2 Row: b Column: 4.
Location/Qualifiers
1. 1539
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                                              CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Blology
http://www.systemsbloigy.org
contact: amadan6systemsbloiogy.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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FQIEETIDRETSGNLEGLLLAVVKSIRSIPATLAYAMKGAGTDDHTLIRVMVSR
SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
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                                                                                                                                                 Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 10 Row: k Column: 21.
Location/Qualifiers
1. .1539
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                            Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Pred. No. 4.1e-242;
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/clone_lib="NHHMGC_17"
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/note="Vector: pOTB7"
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/db_xref-"GI:15215459"
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/db_xref="LocusID:308"
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SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
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Patent: WO 8807576-A 1 06-OCT-1988;
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RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLXDAYELKHALKG
                                                                                                                                                                                                                                                                                                                                                       AGTNEKVLTEIIASRTPEELRAIKOVYEEEYGSSLEDDVVGDTSGYYORMLVVLLQAN
PODPAGIDEAQVEQDAQALEROAGELKAGTDEERFITIFGYSYSHLRKYFDKYMTISG
FOIEETIDRETSGRILAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSR
SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD
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                                                                            Original source text: Homo saplens (clone: PP4-[14,20,26,48].) placenta cDNA to mRNA. Draft entry and computer-readable sequence for [1] kindly provided by U.Grundman, 19-APR-1988. Location/Qualifiers
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Characterization of cDNA encoding human placental anticoagulant protein (PP4): homology with the lipocortin family Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3708-3712 (1988)
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SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURC BASE COUNT	Query J Best Lv Matcher Qy Db	7 8 8 8 8 8	60 60 60	40	3 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
22 ATGGCACGGTTCTCAGAGGCACTGTGACTGCCTGGATTTGATGAGGGGCTGAT 81		AAGGAGACTGGAACAAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA GAACTGAGAGCCATCAAACAACATTATGAAGAAGAATTATTGCTTCAAGGACACCTGAA 	502 AGAGACCTGATGGTGGAATTGATGAAGTTGAACAAGATGAGGCTTTATTT 561 11111111111111111111111111111111111	ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTTTTTTTT	802 GGAGCTGGGACAGATCATCACCTCATCAGAGTCATGGTTTCCAGGAGTGATTGT
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B.P., Pepinsky,R.B. and Browning,J.L. nences, recombinant DNA molecules and prig lippocortins III, IV, V & VI EP 0330396-A2 21 30-AUG-1989; Location,Qualifiers 1. .1432 /organism="unknown" a 276 c 323 9 413 t
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21 from Patent

I07345

RESULT 10 107345 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

Sequence 21 from Pa I07345 I07345.1 GI:590053

253 ATTGTGGCTCTGATGAAACCCTCTGGGCTTTATGATGCTTATGAACTGAAACTTGTGAACTTGTGAAACCTTTGTGAAACCTTTGTGAAACTTGAAAAAAAA	Db 373 GAACTGAGAGCCATCAAACAAGTTATGAAGAATATGGCTCAAGCCTGGAAGTGAC 432	682 ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT	88 81 92 91 12 12 10 10 N	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1454) AUTHORS FUJIKawak. K., Iranl.A.H. and Carter, B.L.A. AUTHORS FUJIKawak. K., Iranl.A.H. and Carter, B.L.A. TITLE HUMAN PROTEINS HAVING ANTICCAGULANT AND ANTI-INFLAMMATORY ACTIVITY JOHNAL PALENT: WO 8805659-A 3 11-AUG-1988. FEATURES Location/Qualifiers Source 1.1454 ACTIVITY ACTIVITY JOHNAN A 279 C 325 9 416 t ORIGIN	Owery Match 97.5%; Score 956.8; DB 6; Length 1454; Best Local Similarity 99.8%; Pred. No. 8.4e+242; Matches 958; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Qy 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGCCTGGATTTGATGAGGGGGCTGAT 81
Qy 862 CTGTTTAACATCAGGAAGAGTTTAGGAAGAATTTTGCCACCTCTTTTATTCCATGATT 921 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 11 HUMATC LOCUS DEFINITION Human placental anticoagulant protein (PAP) mRNA linear PRI 27-APR-1993 DEFINITION Human placental anticoagulant protein (PAP) mRNA, complete cds. ACCESSION M18366.1 GI:179131 ARSTWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (bunata) Eutherist Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1444) AUTHORS Punakoshi,T., Hendrickson,L.E., McMullen,B.A. and Fujikawa,K. TITLE Primary structure of human placental anticoagulant protein JOURNEL Biochemistry 26 (25), 8087-8092 (1987)		// / / / / / / / / / / / / / / / / / /	Oy 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGCTGAT 81	QY 202 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACT

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Web site:

Contact:

Contact:

Insc_mgc@nhgri.nlh.gov
Shevchenko, Y. Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B. Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
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FQIEFTIDRETSGNLEQLLAVVKSIRSIPAYLAETLLYGAMKGAGTDDHTLIRVMVSR
SEIDLENIRREFRKNFATSYSMIRGDTSGDYKKALLLLCGEDD"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 219480.
Location/Qualifiers
                  Euteleostom1;
                                                                    Direct Submission
Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Galthersburg, Maryland:
Web site:
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Catarrhini; Hominidae;
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                                 Primates;
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Mammalia; Eutheria; Primates;
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Strausberg, R.
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/translation-"Maqvlrgtvtdfpgfderadaetlrkamkglgtdeesiltllts
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                                       Direct Submission
Submitted (15-AUG-1988) Hauptmann R., Ernst Boehringer Institut
fuer Arzneimittelforschung, Dr. Boehringer-Gasse 5/11, A-1121 Wien,
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Data kindly reviewed (11-Nov-1988) by Hauptmann
Location/Qualifiers
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124 .132
/note="Kozak consensus (tegecatgg)"
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Pred. No. 8.4e-242;
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1 (bases 1 to 1560)

Maurer-Fogyi., Reutelingsperger, C.P., Pieters, J., Bodo, G., Stratowa, C. and Hauptmann, R.
Cloning and expression of cDNA for human vascular anticoagulant, Cat-dependent phospholipid-binding protein

Eur. J. Biochem. 174 (4), 585-592 (1988)
                                                                                                                                                                                                                                                                                                                           AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA
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X12454. G1:37636
phospholipid-binding protein; vascular and Homo sapiens (human)
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  /product-'human anticoagulant'
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Pred. No. 8.4e-242;
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                      /product='human
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/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="texon:9606"
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                                                                                                                                                                                                                                                                                                                                                             ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT
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20-FEB-1987 JP 87P 3723
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JP 1989020095-A/1
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hypothetical: No;
anti-sense: No;
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JP 1989020095-A/1.
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Search completed: August 28, 2003, 18:14:03 Job time : 2604.33 secs

August 28, 2003, 15:43:40; Search time 2602.33 Seconds (without alignments) 15421.677 Million cell updates/sec 1 atggcatgtggcggtggcca.....tgctctccggagaagatgac 5777422 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 2888711 segs, 20454813386 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 length: 0 length: 2000000000 US-09-970-969-1 981 sed Title: Perfect score: Scoring table: Minimum DB Maximum DB OM nucleic Sequence: Searched: Run on:

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AUTHORS TITLE JOURNAL FEATURES REFERENCE

M21731 Human lipoc J03745 Human endon 107181 Sequence 12 A1845 H.sapiens P A01770 DNA sequenc E14531 CDNA encodi 133411 Sequence 4 107344 Sequence 20 BC018671 Homo sapi D63423 Mouse mRNA AX305384 Sequence U29396 Mus musculu Y11253 O.1atipes m M22248 Bovine endo X13627 Bovine mRNA D78178 Bovine mRNA AX178799 Danio rer A01772 DNA sequenc A01773 DNA sequenc A01774 DNA sequenc Y11253 O.latipes m M19384 Human place
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Unclassified.
1 (bases 1 to 981)
Talt,J.F. and Brown,D.S.
Annexin derivative with endogenous chelation sites
Patent: US 6323313-A 1 27-NOV-2001;
Location/Qualifiers linear DNA 981 bp Sequence 1 from patent US 6323313. AR262469 AR262469.1 GI:28073913 Unknown. RESULT 1
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Tait, J.F. and Brown, D.S.
Annexin derivative with endogenous Patent: US 6323313-A 3 27-NOV-2001,
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Pred. No. 6.6e-248;
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Oy 661 ATGACTATATCAGGATTTCAAATTGAGGAAACCATTGACCGCGGGGACTTCTGGCAATTTA 720	QY 721 GAGCAACTACTCCTTGCTGTAGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAG 780 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 781 ACCCTCTATTATGCTATGAAGGAGCTGGGACAGATCATACCCTCATCAGGAGTCATG 840	Qy 841 GTTCCAGGAGTGAGATTGATCTGTTTAACATCAGGAGGAGTTTAGGAAGAATTTTGCC 900 	OY 901 ACCTCTTTATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTG 960 111111111111111111111111111111111111	Qy 961 CTGCTCTCCGGAGAGATGAC 981 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 3 AR262471 LOCUS AR262471 LOCUS AR262471 P81 bp DNA linear PAT 29-JAN-2003 ACCESSION AR262471 VERSION AR262471 VERSION AR262471.1 GI:28073915	_	REFERENCE 1 (bases 1 to 984) AUTHORS Tait,J.F. and Brown,D.S. TITLE Annexin derivative with endogenous chelation sites JOURNAL Patent: US 6223113-A 5 27-NOV-2001; FEATURES Location/Qualifiers 1981	OUNT 286 a	Query Match 99.5%; Score 976.2; DB 6; Length 981; Best Local Similarity 99.7%; Pred. No. 1.2e-246; Length 981; Matches 978; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 ArGCCATGGGCGGCGCACAGGTCTCAGAGGCACTGCACTCCCT 60 61 GATTGATGGCGGCTGGCACAGGTCTCAGAGGCACTGGACTGCTCCCT 60 Qy 61 GGATTTGATGAGCGGCTGATGCAGAACTCTTCGGAAGGCTATGAAAGCTTGGCCACA 120 61 GGATTTGATGAGCGGCTGATGCAGAACTCTTCGGAAGGCTATGAAAGCCTTGGCCACA 120 Qy 121 GATGAGGAGGCTGATGCAGAACTCTTCGGAAGCTATGAAAACTCTGGCACACACTGCACAGCACACTGACACACAC

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BC004993
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FQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSR
SEIDLFNIRKEFRRNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
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Altachul, S.F., Zeeberg, B. Buetow, K. H., Derge, J. G.,
Altachul, S.F., Zeeberg, B. Buetow, K. H., Schaefer, C.F., Bhat, N. K.
Altachul, S.F., Zeeberg, B. Buetow, K. H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Macca, T. , Wang, J., Halch, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
Scheetz, T. E., Brownstein, M. J., Uddin, T. B., Toshlyuki, S.,
Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A.; McEwan, P. J.,
Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Glbbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madon, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Maden, A., Young, A. C., Shevchenko, Y.,
Butterfield, S. S., Krzywinski, M. I., Skalska, U., Smallus, D. E.,
Schnerch, A., Scheln, J. E., Jones, S.J. and Marra, M. A.
1536 bp mRNA linear PRI 06-JUN-2003
Homo sapiens annexin A5, mRNA (cDNA clone MG:4402 IMAGE:2906015),
complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Strausberg,R.
Direct Submission
Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Emall: cgapbs-remail.nih.gov
Tissue procurement: ATCC/DCTD/DTP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1E. (bases 1 to 1539)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buttow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, R.D., Earmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McErnan, K.J., Malek, J.A., Gunatane, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodisjuez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.J., Schlawood, J., Schwutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.J., Shalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Ghoth, M. Man, A., Man, M. Sodergren, E.D., Muran, and Marra, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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Submitted (15-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC012804.1 GI:15215411
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SEIDLENIRKEFRKRFATSLYSMIKGDTSGYYGKALLLLCGEDD"
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Pred. No. 6.8e-242;
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             sapiens
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llarity 99.2%;
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E 1 (bases 1 to 1539)

S trausberg.R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max.S.I., Wang,J., Hang,J., Hang,J., Hang,J., Blatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunarane,P.H., Richbards,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Wurny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
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FQIEFIDRFTSGNLAVKSIRSIPATLATAMKGAGTDDHTLIRVWSR
SEIDLFWIRKEFRRNFATSLYSMIKGDTSGDYKKALLLLGGEDD"
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                                                CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Blology
http://www.systemsblology.org
contact: amadan@systemsblology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurac
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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                                                                                                                                                                                                                                                                              /organism-"Homo saplens"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Human placenta anticoagulant protein PP4 mRNA, complete cds. M19384 J03545 4 J03544 J03544 J03544 I GI:189614 anticoagulant protein; thromboplastin inhibitor. Homo sapiens (human)
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Grundmann, U., Abel, K.J., Bohn, H., Lobermann, H., Lottspeich, F. and
                            791 ATGCTATGAAGGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGA
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   GCATCCTGACTCTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTT
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RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKG
AGTNEKVLTEITASRTPEELANIKOVYEEFGSSELDDVYGOTSGYYGNELVVLLQAN
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SEIDLFNIRKEFRRNFATSLYSMIKGDTSGDYKKALLLLCGEDD*
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                                                                                                                              Direct Submission
Submitted (15-AGG-2001) National Institutes of Health, Mammaliar
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
             Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Email: cgapbs.remail.nih.gov
Tissue Procurement: ArC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
   Skalska, U., Smailus, D.E.,
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/clone="MGC:4465 INAGE:2961097"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="kHLMGC_17"
/lab_host="DH10B-R"
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Butterfield, Y.S., Krzywinski, M.I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
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/db_xref="LocusID:308"
/db_xref="MIM:131230"
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99.8%; Pred. No. 1.6e-241;
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RSNAQRQEIGAAFKTLFGRDLLDDLKSELTGRFEKLIVALMKPSRLYDAYELKHALKG
AGNEKVLTEITASRTPEELRAIKOYVEEFGSSELEDDVGOTSGYYGNELVVLAAN
RDPDAGIDEAQVEGDAAALFQAGELKWGTDDEEKFTTFGTREVSHLRKVFDKYWTISG
FQIEETIDRETSGNLEOLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVWVSK
Characterization of cDNA encoding human placental anticoagulant protein (PP4): homology with the lipocortin family Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3708-3712 (1988) 88234495 Sel. U.S.A. 85 (11), 3708-3712 (1988) 2967495 Criginal source text: Homo sapiens (clone: PP4-[14,20,26,48].) placenta cDNA to mRNA. Discente chary and computer-readable sequence for [1] kindly provided by U.Grundman, 19-APR-1988. Location/Qualifiers
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/replace="c"
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product = anticoagulant protein 4"
/protein_id="AAB5945.1"
/db_xref="GI:189615"
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97.7%; Score 958.2; DB 9;
Best Local Similarity 99.2%; Pred. No. 6.8e-242;
Matches 963; Conservative 0; Mismatches 8;
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/tissue_type="placenta"
<1. 1582
/product="pp4 mRNA"
151. .1113
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Wallner, B.P., Pepinsky, R.B. and Browning,
Man sequences, recombinant DNA molecules
producing lipocortins III, IV, V & VI
Patent: EP 0330396-A2 21 30-AUG-1989;
                                    Location/Qualifiers
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                                    ATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGGCTGAT
                                            GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGGAGCATCCTGACT
                                                                                CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG
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                                                                                                  CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA
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Unclassified.

I (bases I to 1454)
S Fujikawa,K., Irani,M.H. and Carter,B.L.A.
HWAN PROPEINS HAVING ANTICOAGULANT AND ANT.

Location/Qualifiers
I.0454
I.1454

AL Patent: WO 880559-A 3 11-AUG-1988;

Location/Qualifiers
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Sequence 3 from Patent WO 8805659,
108832.1 GI:588459
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1larity 99.8%;
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RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKG
AGTNEKVLTEITASRFPEELBAIKOVYEEFGSSLEDDVYGOFSGYYORMLVVLLQAN
RDPDAGIDBAQVEQDAQALFYQAGELKWGTDEFKTIFGTRSVSHLKVFDKYWTISG
FQIEFTIDRFTSGNLAVKSTRSIPAYLAFTLYFANKGAGTDDHTLIRVWVSR
SEIDLFNIRKEFRKNPATSLYSMIKGDTSGDYKKALLLLCGEDD"
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Catarrhini; Hominidae; Homo.
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          CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG
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Location/Qualifiers'
1. .1444
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/db_xref="GI:179132"
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/db_xref="taxon:9606"
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/product="ATC mRNA"
13. 975
/note="anticoagulant p.</pre>
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Human placental anticoagulant
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/translation-"MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTS
RSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKG
AGTNERVITEIIASRRPEELAAIKQYYEEFKSELEDDVYGTSGYYQRMLVYLLQAN
RDPDAGIDEAQVEQDAQALFQAGELKWGTDEEKFTIFGTRSVSHSKYFDKYMTISG
FQIEBTIDRETSGNLAQUELAAVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVWYSR
SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
                                                                                                                                                                                                                                                                Web site:

Contact:

Contact:

Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Zhang, L.-H. and Green, E.D.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 219480.
Location/Qualifiers
                Euteleostom1;
                                                                                  Mammalian
                                                                                                 Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Py: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:
nisc_mgc@nhgri.nih.gov/
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Catarrhini; Hominidae;
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Submitted (12-DEC-2000) National Institutes of
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/db.mce.Mgc:2261 IMAGE:3140878
/tissue_type="Ovary, adenocarcinoma"
/clone_lib="NIH_MGC_9"
                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nlh.gov
Context: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP
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Pred: No. 1.6e-241;
); Mismatches 2;
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/protein_id="AAH01429.1"
/db_xref="G1:12655149"
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/mol_type="mRNA"
/db_xref="LocusID:308"
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              Chordata;
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99.8%;
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                                         GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGGAGCATCCTGACT
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/protein_id="CA330985.1"
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/db_xref="G1:37637"
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AGTNEKVLTEIIASRRPFELAIKOVYEEEVESTEDDVVGOTSGYYORMLVVLLQAN
RDPDAGIDEAVVEQULLAVKSIRSIPARTSGTRSVSHLRKVFDYYMTISG
FQIEFTIDREFGSNLFQLLLAVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSR
SEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGEDD"
          Hauptmann, R.
Birect Submission
Submitted (15-AUG-1988) Hauptmann R., Ernst Boehringer Institut
fluer Arznelmittelforschung, Dr. Boehringer-Gasse 5/11, A-1121 Wien,
Austria
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/db_xref="txxn:9606"
/clone="lambda pl1/3 and others"
/tissue_type="placental"
124. .132
/note="Kozak consensus (tcgccatgg)"
129. .1091
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/note="structural repeat (67 AA)"
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                                                                                                                                                                                                                                                   /note-"VAC protein (AA 1-320)"
                                                                                              Data kindly reviewed (11-Nov-1988) by Location/Qualifiers
1. 1560
/organism="Homo_sapiens"
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Catarrhini; Hominidae; Homo.
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1 (bases 1 to 1560)
Maurer-Fogy,I., Reutelingsperger,C.P., Pieters,J., Bodo,G., Stratowa,C. and Hauptmann,R.
Cloning and expression of cDNA for human vascular anticoagulant, Ca2+-dependent phospholipid-binding protein
Eur. J. Blochem. 174 (4), 585-592 (1988)
                           GGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT
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1 X12454
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phospholipid-binding protein; vascular an Homo sapiens (human)
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CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATT 921
                       anticoagulant mature peptide
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                                                                                                                          Length 1566;
   F
   /product - 'human anticoagulant'
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                                                                                                                        Score 956.8; DB 6;
Pred. No. 1.6e-241;
); Mismatches 2;
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                      /product-'human
                                                                                            447
                                                           /organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
                             1099, .1566.
Location/Qualifiers
1. .1566
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Best Local Similarity 99.8%;
Matches 958; Conservative
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20-FEB-1987 JP 87P 37227
SAINO SUKEYUKI, IMASAKI AKIO, SUDA MAKOTO
CI2P21/02,C07K13/00,C12N15/00//A61K37/02,(C12P21/02,C12R1:19);
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                                                                    AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT 561
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Salno,S., Iwasaki,A. and Suda,M.
POLYPEPTIDE HAVING ANTI-BLOOD COAGULATING ACTION
Patent: JP 1989020095-A 1 24-JAN-1989;
                                                                                                                                                                                                                                   CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA
                                                                                                                                                                                                      CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA
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                                                                                                                                                                                                                                                                                                                  CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATT
                              GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type=placenta;
clone=pMKT7;
                                                                                                                                                                                                                                                                                                                                                                                                                             E01816 1566 bp cDNA encoding human anticoagulant.
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136. .1098
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JP 1989020095-A/1
24-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          topology: Linear;
hypothetical: No;
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Homo sapiens (human)
Homo sapiens
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E01816
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KEYWORDS
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	recrectores and a second secon	GCTGCTCTGGAGAAGATGAC 1095	
	922 AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGAC 981	1036 AGGGGGGTACATCTGGGGACTATAGAAAGCTCTTCTGCTGTGTGTG	Search completed: August 28, 2003, 18:14:01 Job time : 2606.33 secs
976	922	1036	Search completed: August Job time : 2606.33 secs
qa	οy	q	Sea

Fri

Scoring table:

Searched:

Database

Perfect score: Sequence:

OM nucleic

Run on:

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BX398791 BX398791
BX396240 BX396240
BX396240 BX396240
BX358605 BX386605
BX402751 BX402751
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BX402751 BX402751
AL517516 AL517516
AL547761 AL547761
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BX40530 BX365074
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BX461471 BX461471
BU1671.99 AGENCOURT
BQ877512 AGENCOURT
BG392737 GO2410103
BG767111 G0274 0475
BX397346 BX397346
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BX377166 BX377166
BM016480 603641294
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg.R.
Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Contact: MGC help desk
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Homo sapiens, clone IMAGE:3924873, mRNA.
BC032093
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BX424940
BX399821
AL537256
AL557433
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BU368794
BU229583
AL514020
BX381687
BX460530
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BX395533
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BX461471
BU167199
BQ877512
BG392737
BG767111
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BX377166
BM016480
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777.3
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TITLE
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COMMENT
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 BC032093 Homo sapi
BM464122 AGENCOURT
BX441583 BX441583
BX379189 BX379189
                                                                                          (without alignments)
14228.779 Million cell updates/sec
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                                                                             August 28, 2003, 15:48:20 ; Search time 1675.67 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                              1 atggcatgtggcggtggcca.....tgctctccggagaagatgac
                                                                                                                                                                                                                                 45562784
          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                         22781392 seqs, 12152238056 residues
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Maximum Match 100%
Listing first 45 summaries
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BM464122
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BX379189

    nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0
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em_gss_vrl:*
gb_gssl:*
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Maximum DB seq length: 200000000
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em_gss_vrt:*
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em_gss_rod:*
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gb_est5:*
em_estfun:*
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87.5
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22243211114711168
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HTC 06-JUN-2002

958.2 874.4 868.6 858.4

Score

Result ě

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1076 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6445585 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5540173
5, mRNA sequence.
                                                                                                                                                                                                                                         984 GTGAGATTGATCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTTT 1043
                                                                                                                                                                                                                                                                                                     1044 ATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTGTG 1103
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/mol_type="mRNA"
/mol_type="mRNA"
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/clone="IMAGE:5540173"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic plane"
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/clone=lin="NIH_MGC_72"
/note="organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Site_2: sali; Cloned unidirectionally. Primer: Oligo dT.
Perhologies :
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NIH-WGC http://mgc.ncl.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI2235 row: n column: 14
High quality sequence stop: 708.
      804 CAGGATTTCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTAC
                                         105 AIGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGGGGGTGAT
                                                                                                                                                                                                                                                                                  911 ATTCCATGATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCG
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Pred. No. 2.2e-223;
0; Mismatches 25;
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96.9%;
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Best Local Similarity 96.9
Matches 932; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                   Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 26 Row: f Column: 11
This clone has the following problem: no 5' EST match.
                      Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 GCGGTGGCCATATGGCACAGGTTCTCAGAGGCACTGTGACTGCCTTCCCTGGATTTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 TIGAAAARTIAATIGIGGCICIGAIGAAACCCICICGGCITIAIGAIGCITAIGAACIGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 AGCCTTTATTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCA
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                                                                                                                                                                                                                                     /organism-"Homo saplens"
//mbl type="mRNA"
//db_xref="taxon:9606"
/clone="IMAGE:3924873"
/clone="IMAGE:3924873"
/clone=11b-"NHL_MGC_72"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Indels
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Pred. No. 9e-246;
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
337 c 364 g 452 t
                                                                                                                                                                                                      Location/Qualiflers
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Best Local Similarity 99.2%;
Matches 963; Conservative
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                                                                                                                                                                                                                                                                                      /cione="CSODPG19KK1"
/tissue_type="FETAL BRAIN"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

a 229 c 274 g 272 t 5 others
                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr /
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgl?seq-cSODF019AF060P16cluster=2353.r. Contact :
Feng Liang Email: fliangflifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF019AF060P1.
                                Euteleostom1;
                                                                                                                                                       For
                                                                                                                                                                                       Contact
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                                           Catarrhini; Hominidae;
                                Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 868.6; DB 13; Length
Pred. No. 8e-222;
1; Mismatches 11; Indels
                                                                and Polayes, D. normalization
                                                                 and
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                      Homo sapiens
Eukaryota; Metazoa; Chordata; Cra
Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 1071)
Li,W.B. Gruber,C., Jessee,J. and
Full-length cDNA libraries and no
Unpublished
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ilarity 98.6%;
Conservative
           sapiens (human)
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        GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT
                                                   GAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC
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                                                                                              ATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG
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                                                                      GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCCTTCAGGCTAAC
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                                                                                                                                            263 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         983 GGAGCTGGGACAGATGATCATACCCTCAWCAGAGTHATGGKTTCMAGGAGTGAGATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
 Length 1201;
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            Pred. No. 4.7e-219;
87.5%; Score 858.4; 94.9%; Pred. No. 4.70
                             Conservative
               Similarity
               Best Local Sim:
Matches 892;
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/primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
263 c 295 g 294 t 42 others
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BX379189 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODIO30YLL8 5-PRIME, mRNA sequence.
BX379189.1 GI:30446777
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Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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BP 191 91006 EVRY cedex - France
Bmall: segrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
egi-bin/cluster.cgi?seq-CS0D1030DF09QPl&cluster-2353.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0DI030F09QPl.
                                                                                                                                            CAGGATTTCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTAC
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                                                                                                                             TCTTTGGAACACGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATAT
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BX398791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COT 25-NORMALIZED Homo sapiens CDNA CLORE CSODIO64YH19 5-PRIME, mRNA sequence.

BX398791

BX398791. GI:30613780
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BP 191 91006 EVRY cedex - France
Bmall: sequencscope.cns.fr Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
Invitrogen. This sequence belongs to sequence cluster 2353.r For
Invitrogen.cns.fr/
cgi-bin/cluster.cgi?seq-cS0D1064CD10QP16cluster-2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1064CD10QP1.
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// Organism="Homo saplens"
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// Aba_rref="Laxon:9606"
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// Clone="Lib="Homo saplens PLACENTA"
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I. ihrarv was not normalized."
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Genoscope - Centre National de Sequencage
Br 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                            http://www.genoscope.cns.fr/
cgi.bin/cluster=2353.r. Contact
cgi.bin/cluster.cgi?seq=CSODE009BE08OP1&cluster=2353.r. Contact
Feng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE009BE08QP1.
Location/Quallifiers
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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mRNA sequence.
                                                                                Homo sapiens (human)
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/ Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="RAM"
// Organism="MARA"
// Organism="MARA"
// Organism="Laxon:9606"
// Clone="CSODIO147109"
// Clone="Lype="PLACENTA COT 25-NORMALIZED"
// Clone="Late "Homo sapiens PLACENTA COT 25-NORMALIZED"
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// Orde="late item of sapiens place with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMYSPORT 6 vector. Library was normalized."

35 a 234 c 272 g 270 t lothers
1062 bp mRNA 11near EST 13-MAY-2003
BX396240 Homo saptens PLACENTA COT 25-NORMALIZED Homo saptens CDNA
CLORD CSODIO14Y109 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                       Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-CSODI014AE050Pl&cluster=2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI014AE050Pl.
Location/Qualifiers
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                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1062)
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Pred. No. 2.4e-216;
1; Mismatches 4; Indels 0;
                                                                                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
                                                                        BX396240.1 GI:30624830
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llarity 99.4%;
Conservative
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Homo sapiens
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                primer. Five prime end enriched; double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCNVSPORT 6 vector. Library was normalized.
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15; Mismatches 5;
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BX379218 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO31YA16 5-PRIME, MRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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cg1.bin/cluster.cg1?seq=CSOD1031BA0BQPl&cluster=2353.r. Contact
Feng Liang Fmail: filang@lifetech.com/RL:
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI031BA0BQPI.
Location/Qualifiers
                                                                                                                                                    AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
                                                                CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA
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BP 191 91006 EVRY cedex - France
Emall: seqreféqenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r.
more information about this cluster, see
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/mol_type="mRNA"
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/clone="CS0DI031xA16"
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSOD1041BE010Plscluster=2353.r. Contact:
Feng Liang Email: filang@lifetech.com URi:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI041BE010Pl.
Location/Qualifiers
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BX38605 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSODI041X102 5-PRIME, mRNA sequence.
BX358605
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1 (bases 1 to 1076)
14, W.B.; Gruber, C.; Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                        AATTGAGGAAACC - ATTGACCGCGAGACTTCTGGCAATTTAGAGCCAACTACTCCTTGCTG
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/do.tref="textor:9606"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
Library was not normalized."
10 a 243 c 293 g 307 t 48 others
                                                                                                                                                                                                                                                                      On Feb 15, 2001 this sequence version replaced gi:12874598.

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr.
cgi.bin/cluster.c37seq-C30bE012BE07QP1&cluster-2353.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0bE012BE07QP1.
                 AL542496
AL542496 Homo saplens PLACENTA Homo saplens cDNA clone CSODE012x114 5-PRIME, mRNA sequence.
AL542496.2 GI:30547699
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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98.2%; Pred. No. 1.1e-213;
11ve 3; Mismatches 10;
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized. 233 c 274 g 278 t 4 others
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                                                   Score 835.8; DB 13; Length
Pred. No. 5.1e-213;
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RESULT 11 BX402751

Location/Qualifiers

1. 1007
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO84YA05"
/clone="CSODIO84YA05"
/clone="Lb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_lb="Homo sapiens"
/clone_lb="Homo s ö EST 13-MAY-2003 141 290 201 261 410 321 381 530 590 OT 25-NORMALIZED Homo sapiens CDNA Argecacagetrereaaggeactereacteceregatrreargagegegerear 230 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1853.r For more information about this cluster, see
http://www.genoscope.ns.fr/
cgi-bin/cluster.cgi?seq=CSIAI0212G030P16cluster=2353.r. Contact :
ferge Liang Email : fliangelifeteen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSIAI0212G03QP1. 81 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1007)
1 (Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished 231 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCCACAGATGAGGAGCATCCTGACT AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA ATGCCACAGGTTCTCAGAGGCACTGTGACTGCCTTCCCTGGATTTGATGAGCGGGCTGAT GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG ATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG GAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC Gaps ö Length 1007 Indels Score 832.2; DB 13; Pred. No. 4.6e-212; 0; Mismatches 3; DX402751 Homo sapiens PLACENTA COT 25-NORA CIONE CSODIO84YA05 5-PRIME, MRNA sequence. 1007 bp BX402751.1 GI:30607254 84.8%; 99.6%; Homo sapiens (human) Homo sapiens Contact: Genoscope 834; Conservative Similarity 277 Query Match Best Local Si Matches 834; 82 142 202 22 291 351 262 411 322 382 471 531 BASE COUNT ORIGIN DEFINITION ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS SOURCE FEATURES ò q ŏ g δ g δ 셤 ò g QY qq ò g

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AL517516 1201 bp mRNA linear EST 12-MAY-2003
AL517516 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone
Query Match
Best Local Similarity 95.0%
Matches 911; Conservative
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// Organism="Homo sapiens"
// Mol_type="mRNA"
// Mol_type="mRNA"
// Ab xref="taxon:9606"
// Clone="CSDI017YJ11"
// Lissue_type="PlacENTA COT 25-NORMALIZED"
// Clone_lib="Homo sapiens PlacENTA COT 25-NORMALIZED"
// Orde="let strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

11 a 252 c 305 g 306 t 27 others
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On Feb 15, 2001 this sequence version replaced gi:12882128.
Contact: Genoscope
Genoscope
Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgl?seq-CSOD1017CE060Plscluster=2353.r. Contact:
Feng Lidng Email: fliang@lifetech.com URL:
http://tullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOD1017CE060Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL547761 1201 bp mRNA 11near EST 31-MAY-2003
AL547761 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI0177311 5-PRIME, mRNA sequence.
                                                                           ATTGAGGAAACCATTGACCGCGAGACTTCTGCCAATTTAGAGCAACTACTCCTTGCTGTT 741
                                                                                                                                                                                                                                                                         ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT 890
                                                                                                                                                                                                                                                                                                                     561
                                                                                                                      CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA 621
                                                                                                                                                                                 CGAAGIGIGICICATITGAGAAAGGIGITIGACAAGIACAIGACIAIAICAGGAITICAA 681
                                                                                                                                                                                                                                                                                                      GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGAAG 801
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                                                                                                                                                                                                                                                                                                                                                                              GGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATT 858
                                                            AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
 GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCTCTTCAGGCTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL547761.2 GI:31269590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                  22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT
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                                                                                                                                                                                                             AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA
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                   11;
 Length
                   Indels
                   26;
; Score 831.6; DB 9,
; Pred. No. 7.3e-212,
11; Mismatches 26;
 84.8%;
95.0%;
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AL541412 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE006YJ10 5-PRIME, mRNA sequence.

AL541412. GI:30545565
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (hases I to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full.length cDNA libraries and normalization

Unpublished

On Feb 15, 2001 this sequence version replaced gi:12872460.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-CSODEO06DE05OP1&cluster-2353.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODEO06DE05QP1.
                                                                                                                                                                                                   TCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                            ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT
                    GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC
                                                                     AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGC 961
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/clone="CSODE006yJ10"
/tissue_type="PLACENTA"
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sapiens
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/db_xref="taxon:9606"
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/clone=lb="Homo sapiens NEUROBLASTONA"
/note="Yector: pcMYSPORT_6; lst strand cDNA was primed
/note="Yector: pcMYSPORT_6; lst strand cDNA was primed
/vith a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMYSPORT 6 vector.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
On Feb 13, 2001 this sequence version replaced gi:12781009.
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                                                                                                                                                                                                                               Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BMail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cg1?seq-CSODA003CC03QPl&cluster-2353.r. Contact :
Feng Liang Email: fliang@lifetech.com UR. :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODA003CC03QPl.
Location/Qualifiers
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6
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CSODA003YF05 5-PRIME, mRNA sequence.
AL517516
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                                 AL517516.2 GI:30534896
                                                                  sapiens (human)
                                                                                   Homo sapiens
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860

Euteleostom1; Homo.

g1:12952676

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mRNA linear EST 13-MAY-2003
Homo sapiens CDNA clone CSODE004YD21
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2383.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODE004CBI1QP16cluster=2353.r. Contact
Feng Liang Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE004CBI1QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG
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                                                                                                                                                        Cranlata; Vertebrata; E
Catarrhini; Hominidae;
                                                                                                                                                                                                                  2001 this sequence version replaced
                                                                                                                                                                       1 (bases 1 to 1022)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
               ATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTC
                                                                                                                                                                                                                            Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 820.4; DB 9;
Pred. No. 6.7e-209;
5; Mismatches 1;
                                                                                AL583578 Homo sapiens PLACENTA
5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates;
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99.1%;
                                                                                                                                    sapiens (human)
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/clone_lib="Homo sapiens PLACENTA" hote="Vector: pCMYSPORT_6" ist strand cDNA was primed with a NotI-ollgo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecory sites of the pCMVSPORT 6 vector.
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Search completed: August 28, 2003, 19:38:11 Job time : 1681.67 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein August 22, 2003, 21:27:21 ; Search time 37.6667 Seconds Run on:

(without alignments)
1377.971 Million cell updates/sec

1 MACGGGHMAQVLRGTVTDFP.......KGDTSGDYKKALLLLSGEDD 327 Sequence:

US-09-970-969-2 1639 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 Total number of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Modified human ann	Modified human ann	Modified human ann	Placental coaqulat	Vascular anti-coaq	PAP-I. Homo sapie	S65T GFP variant/h	Amino acid sequenc	Human annexin V, c
		ΙD	AAB50863	AAB50865	AAB50864	AAP80511	AAP91953	AAR13082	AAY13923	AAY84788	ABG31220
		90	22	22	22	σ	10	12	20	77	23
		Match Length DB ID	327	327	327	320	320	320	320	320	320
9	Query	Match	100.0	99.2	98.7	97.0	97.0	97.0	97.0	97.0	97.0
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anticoagulant PP4	PAP-I isolated fro	CPB-I. Homo sapie	Calphobindin I (CP	Human CPB-1 protei	Sequence vascular	Sequence vascular	Vascular anticoagu	CPB-1. Homo sapie	ij	CPB-1. Homo sapie	S65T GFP variant/h	Mouse ischaemic co	S65T GFP variant/h	Rat annexin-V. Ra	Human annexin V pr	Modified annexin p	Lung cancer assoct	Human placenta-der	Human NOVX polypep	Human placenta-der	S65T GFP variant/h	Human ovarian canc	Human cancer assoc	Anticoagulative PP	Amino acid sequenc	n diac	Annexin XI type I	Annexin XI type I	Lung cancer associ	Human polypeptide	-	an	VAC-beta. Synthet	Human protein SEQ
AAP90053	AAP82317	AAR26276	AAR41021	ABG32550	AAP80242	AAP80714	AAR11910	AAR26180	AAP91363	AAR25718	AAY13924	ABB57067	AAY13925	AAR75695	ABP56248	ABP56249	AAB58393	AAR03725	ABU54621	AAR03726	AAY13926	ABG96279	AAB43617	AAP91913	AAY84790	ABG19948	AAR34127	AAR34128	AAY07117	ABP69394	AAP80715	AAP91954	AAR35754	AAM78665
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96.8	96.8	2.96	7.96	2.96	96.6	9.96	9.96	96.4	96.2	94.8	90.3	90.3	88.8	88.4	88.0	88.0	61.7	56.9	56.9	56.8	56.3	56.3	56.3	56.3	55.3	53.2	52.8	52.3	52.2	51.5	50.7	50.7	50.7	50.7
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ALIGNMENTS

Human; annexin; chelation site; nuclear imaging; apoptosis; transplant rejection. Modified human annexin, SEQ ID NO: 2. AAB50863 standard; Protein; 327 AA. 16-MAR-2001 (first entry) WO200073332-A1. Homo sapiens 07-DEC-2000. AAB50863; RESULT 1

25-MAY-2000; 2000WO-US14324. 990S-0324096 (UNIW) UNIV WASHINGTON Tait JF, Brown DS; 01-JUN-1999;

Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid

WPI; 2001-080465/09. N-PSDB; AAC91368.

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                                            chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaginary associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin bloactivity. It can be readily prepared in high radiochamical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.
                                                                                                                                                                                                                                                                                           QDAQALFQAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNL
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                                    present sequence is a modified annexin having an N-terminal
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                                                                                                                                                                    Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; annexin; chelation site; nuclear imaging; apoptosis;
transplant rejection.
extension which comprises a glycine and a cysteine residue
                                                                                                                                                                   100.0%; Score 1639; DB 22; Length
100.0%; Pred. No. 1.1e-142;
.ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       Modified human annexin, SEQ ID NO: 6
                   Page 30-31; 39pp; English.
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nes 327; Conservative
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                                                                                                                                                                                                                                           The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombior apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radiouncide and retain annexin bloactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In other to conventional conjugation chemistries that provide a distribution of conjugation the modified annexin has a single chelation site remote from the site of biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IASRTPEELRAIKOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QDAQALFQAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MACGCGHMAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEI
                                                                              Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid extension which comprises a glycine and a cysteine residue -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 327;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1630; DB 22;
Pred. No. 7.7e-142;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TSLYSMIKGDISGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified human annexin, SEQ ID NO: 4.
                                                                                                                                                                                            Claim 18; Page 37-38; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.5
Best Local Similarity 99.7
Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transplant rejection
WPI; 2001-080465/09.
N-PSDB; AAC91370.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 AA;
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Homo sapiens
                             EP279459-A.
JP03219875-A
                                                                                19-FEB-1988;
                                                                                                               23-JUL-1987;
                                                                                                     20-FEB-1987;
                                                             24 - AUG - 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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ID AAP9
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AC AAP9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         IASRTPEELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQLILAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFA 300
                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                          The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radiounclide and retain annexin bloactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.
                                                                                                                                                                                                                                                                                                                                                                  1 MACGGGHMAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEI
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation inhibitor; disseminated vascular coagulation;
                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                              apoptosis, has N-terminal chelation site comprising amino acid
extension which comprises a glycine and a cysteine residue
                                                                                                                                                                                                                                                                                                                Length 327;
                                                                                                    Novel modified annexin useful for imaging vascular thrombi
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                               Score 1618; DB 22;
Pred. No. 9.8e-141;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 TSLYSMIKGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSLYSMIKGDTSGDYKKALLLLSGEDD 327
                                                                                                                                           Claim 15; Page 33-35; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Placental coagulation inhibitor.
                                                                                                                                                                                                                                                                                                              98.78;
         99US-0324096
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(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                        al Similarity 99.4
325; Conservative
                             (UNIW ) UNIV WASHINGTON.
                                                                     WPI; 2001-080465/09.
                                                  fait JF, Brown DS;
                                                                                                                                                                                                                                                                                         327 AA;
                                                                               N-PSDB; AAC91369
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10-MAR-2003
12-NOV-1990
         01-JUN-1999;
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                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                    This polypeptide exhibits strong anticoagulant activities and is useful for the treatment and prevention of e.g. thrombosis or disseminated intravascular coagulation in the brain, heart and peripheral blood vessels, such as cerebral and myocardial infarction. It has no antigenicity against man and can be produced in large amts. using recombinant methods.

(Updated on 15-MAR-2003 to add missing OS field.)

(Updated on 25-MAR-2003 to correct PF field.)

(Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                     Recombinant placental coagulation inhibitor - useful for the prevention and treatment of thromboses or disseminated intra-vascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.0%; Score 1590; DB 9; 99.7%; Pred. No. 3.6e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                    Disclosure; Page ?; ?pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP91953 standard; protein; 320
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88EP-0102468
                                       87JP-0037227
                                                          87JP-0184428
                                                                                                                                             Suda
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Best Local Similarity 99.7
Matches 319; Conservative
                                                                                                                                           Saino Y, Iwasaki A,
                                                                                                                                                                                    WPI; 1988-236733/34.
WPI; 1991-329110/45.
                                                                                                    KOWA ) KOWA CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 AA;
                                                                                                                                                                                                                             N-PSDB; AAN81113.
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K; PBP;

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61 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence, or a fragment of it, is used in the construction of hybrid phospholipid-binding proteins (PBP) comprising at least one lipocortin phopholipid binding domain (PBD), e.g. of PAP-I, joined activated domainless vitamin K-dependent protein, e.g. protein C or activated protein C. See AAQ12680-81 for such examples. See also AAQ12678-81. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant produ. of hybrid phospholipid-binding proteins comprising lipocortin phospholipid-binding domain and vitamin K-dependent protein
                                                                                                                                                                                                                                                                 Phopholipid; binding protein; lipocortin; domain; vitamin gla-domain; VKDP.
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Pred. No. 3.6e-138;
0; Mismatches 1;
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                       301 KGDTSGDYKKALLLLCGEDD 320
   KGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 7; 57pp; English.
                                                                                                                    AAR13082 standard; Protein; 320
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Best Local Similarity 99.7%;
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               90WO-US07335.
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                                                                                                                                                                                   (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1991-222905/30.
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                                                                                                                                                                                                                                                                                                                   Homo saptens.
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30-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This vascular anti-coagulating protein (VAC)-alpha is used in the preparation of monoclonal antibodies (MAbs). The VAC-alpha is injected into a host animal, in conjugation with eap keyhole limpet heamocyanin, and the B-cells from immunised hosts are then fused with myeloma calls. The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-abpha. Abs can be used as immunossay reagents to detect VAC proteins, as affinity ligands for protein purifico, and as medicaments for binding and/or neutralising VAC proteins in vivo. See also AAN91354 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
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                                                                                                 Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibodies to vascular anti-coagulating proteins hybridomas producing such antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 10-MAR-2003 to add missing OS fleld.) (Updated on 25-MAR-2003 to correct PA fleld.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1590; DB 10;
Pred. No. 3.6e-138;
0; Mismatches 1;
                                                                                                                                                                               Location/Qualifiers
1..320
/product=VAC-alpha protein
                                                                Vascular anti-coagulating protein-alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; fig 1; 11pp; German
                                                                                                                                                                                                                                                                                                                                                                             (BOEH ) BOEHRINGER INGELHEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.0%;
99.7%;
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 (updated)
(updated)
(first entry)
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                                                                                                                                 - Homo sapiens
- Mus musculus
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N-PSDB; AAN91353.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 AA;
25-MAR-2003
10-MAR-2003
30-JUL-1989
                                                                                                                                                                                                                                                                                                               26-MAR-1988;
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                                                                                                                                                                                                                                                DE3810331-A
                                                                                                                                                                                                                                                                               05-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                             Gunther A;
                                                                                                                                Chimeric
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Length 320;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-APR-2000
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The proteins are bifunctional Aequorea victoria green fluorescent protein consists of the protein are bifunctional Aequorea victoria green fluorescent proteins. Where the GFP and annexin moleties provide greater or equal fluorescent intensity and anionic phospholipid binding affinity, respectively, than do the corresponding unfused GFP and annexin proteins. An early manifestation of apoptosis is the loss of the proteins. An early manifestation of apoptosis is the loss of the proteins. The GFP-annexin V fusion proteins are used for the clasma membrane. The GFP-annexin V fusion proteins are used for the detection of apoptotic cells by flow cytometry or fluorescent microscopy. The fusion proteins provide for homogeneously labelled annexin, with fluorescence properties that do not change upon binding membrane phospholipids, unlike prior art FITC-labelled annexins, where quenching of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
 248 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
             Gaps
                                                                                                                                                                                                                                                                  GFP; green fluorescent protein; annexin; fusion protein; apoptosis; fluorescent intensity; anionic phospholipid binding affinity; asymmetric distribution; plasma membrane phospholipid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bifunctional fusion protein useful for the detection of apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 3.6e-138;
); Mismatches 1;
                                                                                                                                                                                                                                      S65T GFP variant/hAnnexin V protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 14-15; 23pp; English,
                                                                                                                                                     AAY13923 standard; protein; 320 AA
                                                      KGDTSGDYKKALLLLSGEDD 327
                                                                      301 KGDTSGDYKKALLLLCGEDD 320
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                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                 apoptotic cell detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-277634/23.
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                                                                                                                                                                                                                                                                                                                                           Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319;
                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                                                                                                                                   AAY13923;
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                                                       308
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Best Local S
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemical
                                                                                                                              ELRAIKOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                Chemical structure having affinity for phospholipid comprises chemical platform comprising six residues supporting set of chemical functions that are capable of binding to phospholipid -
                                                                                                                QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an annexin polypeptide. The domain of annexin, which may be modified, is used to construct the chemical compounds of the invention. The specification describes chemical compounds which have an affinity for a phospholipid. The chemical compounds which have an affinity for a phospholipid. The chemical compounds comprise at least one chemical platform comprising six residues supporting a set of chemical functions that are capable of binding to the phospholipid at least partly define the affinity of the structure for the phospholipid. The compounds act as phospholipid sequesters. The compounds are useful for preparing antithrombotic, antitumor and antinilammatory medicaments, for making coatings for thrombogenic biomaterials, and for preparing labelling compounds useful for analysing and detecting negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guerois
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                                                                                                                                                                                                                                                                                                                                                                   AAY84788 standard; peptide; 320 AA.
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(UYPA-) UNIV CURIE PARIS VI P & M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "domain 1"
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                                                                                                                                                                                                                                                                                KGDTSGDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of annexin V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Fig 6b; 63pp; French.
                                                                                                                                                                                                                                                  KGDTSGDYKKALLLLSGEDD
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deltaV1-5 or their

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pseudo-delta receptors for activated C-kinase (RACK),
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01-NOV-1989
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                                                                                                                                                                                   Sequence
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AAP90053
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                                                                                                                                                                                                                              VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                        ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 187
                                                                           29
                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         damage to
by stroke,
                                                                                                                                                                                                                                                                                                                                                                                                              Human; annexin V; delta RACK; delta protein kinase C; deltaPKC; VI domain; vasotropic; cerebroprotective; deltaV1-1; deltaV1-2; RACK; pseudo-delta receptor for activated C-kinase; deltaV1-5; PKC; protein kinase C; signal transduction; cell growth; gene expression; ion channel activity; translocation; hypoxia; stroke; ischaemic damage; creatine kinase.
                                                                                      MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                               FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                                                                                                                         QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                         Gaps
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                                      Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New delta protein kinase C peptide for reducing or enhancing cells or tissues exposed to ischemic or hypoxic event caused or for protecting tissue from damage due to ischemia -
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                             Human annexin V, containing a delta RACK binding site.
charges on cell surfaces and microvesicles in blood.
                                Score 1590; DB 21;
Pred. No. 3.6e-138;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 45; Page 64-65; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                     ABG31220 standard; Protein; 320 AA
                                                                                                                                                                                                                                                                              11111111111111 1111 320.
                                                                                                                                                                                                                                                                    KGDTSGDYKKALLLLSGEDD 327
                                   97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001; 2001US-262060P
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                  Query Match
Best Local Similarity 99.7
Matches 319; Conservative
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                  320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mochly-Rosen D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200257413-A2.
                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                  Sequence
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derivatives or fragments. Protein Kinase C (PKC) is a key enzyme in signal transduction involved in a variety of cellular functions including cell growth, regulation of gene expression and ion channel activity. The coll growth, regulation of gene expression and ion channel activity. The coll growth, regulation of dense expression and ion channel activity. The coll station of different PKC isozymes to different areas of the cell in coll molecules (RACKS). Peptides that minic either the PKC-binding site on RACKS or the RACK binding site on PKC are isozyme specific activating or inhibitors of PKC. The disclosed peptides are useful in activating or inhibiting translocation or function of deltaPKC. The deltaPKC agonists or antagonists are useful in reducing, enhancing or protecting against damage to cells or tissues due to ischaemic or hypoxic event caused by stroke. Acute administration of the peptides, conjugated to a carrier peptide or a Tat-derived peptide, protected hearts against ischaemic damage as shown by decreased release of creatine kinase. The data indicate that in an inteact heart, inhibition of deltaPKC conferred greater than 50% protection against ischaemic damage. The sequence greater than a namexin V, which contains a delta RACK binding site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEITASRTPE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELRAIKQVY EEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.0%; Score 1590; DB 23; Best Local Similarity 99.7%; Pred. No. 3.6e-138; Matches 319; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anticoagulant; PP4 protein; thromboplastin.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human).
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Annexin V, which has high affinity for active thrombocytes, is used as a carrier molecule to build a thrombus-trageting thrombolytic fusion protein. The protein (this sequence) is the result of expression of a fusion gene comprising the Annexin V gene and a low-molecular urokinase gene, in insect cells. The Annexin V-scu-Ph-32 fusion protein, expressed in insect cells train The Annexin V-scu-Ph-32 fusion protein, expressed and has the fibrinolytic activity of urokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                         protein for targetting thrombus - comprises urokinase
                                                                                                                                                                                                                                                                                                                                             Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAP-I; anticoagulant; anti-inflammatory agent; phospholipid; phospholipase A2; disseminated intravacular coagulation; deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAP-I isolated from biological fluid, used as anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                            96.8%; Score 1587; DB 21;
99.4%; Pred. No. 1.7e-137;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                 Claim 2; Page 2-4; 20pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP82317 standard; protein; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88WO-US00340.
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(first entry)
                                                                                                                                                                                                                                                                                                                                               Query Match 96.85
Best Local Similarity 99.45
Matches 318; Conservative
                                                                                               New thrombolytic fusion fusion of Annexin V and
                  Yang G;
                                               WPI; 2000-413098/36
                                                                                                                                                                                                                                                                                                               600 AA;
                                                                 N-PSDB; AAA11241
                  Sun J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1988;
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13-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308
                                                                                                                                                                                                                                                                                                                  Sequence
                 Wu Χ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
                                                                                                                                                                                                                                                                                                                                                                                                              1 MAQVLRGTVTDFPGFDERADAQTLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein; urokinase; insect cell; fibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                Length 320;
                                                                                              New DNA sequence encoding anticoagulant PP4 protein - and new recombinant protein, vectors, antibodies, etc., useful therapeutically and diagnostically.
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                            Amino acid sequence of anticoagulant PP4 protein. This inhibits blood coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                            Score 1587; DB 10;
Pred. No. 6.9e-138;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                               Claim 1; page 11 and Table 1; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Annexin V/urokinase fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGDTSGDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGDTSGDYKKALLLLSGEDD 327
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                                  Kupper
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY92930 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99CN-0113524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99CN-0113524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
(BEHW ) BEHRINGWERKE
                                                             WPI; 1989-166767/23
                                                                                                                                                                                                                                                                                            320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jnidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-2000
                                                                                                                                                                                                                                                                                               Sequence
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RESULT 11 AAY92930

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69 GRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                                                                                                                                                                                                                                                                  The sequence given is the amino acid sequence of CPB-I. CPB-I was used within a method which involved adding basic amino acids to it which resulted in its stabilisation. This lead to the production of CPB-I which keeps its activity when it is frozen, molten or has been processed by several procedures. (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 319;
                                                                                                                                                                                                                      Stabilisation of CPB-1 for drug compsn. - by adding basic aminoacid selected from lysine, arginine and/or ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 96.7%; Score 1585; DB 13; Best Local Similarity 99.7%; Pred. No. 1e-137; Matches 318; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR41021 standard; protein; 319 AA
                                                                                                                                     (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
(KOWA ) KOWA CO LTD.
                                                                                                                                                                                                                                                                        Disclosure; Page 2; 4pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDTSGDYKKALLLCGEDD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDTSGDYKKALLLLSGEDD 327
                                                                   90JP-0328286
                                                                                                    90JP-0328286
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                                                                                                                                                                                     WPI; 1992-288937/35
                                                                                                                                                                                                                                                                                                                                                                                                                        319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calphobindin I
     JP04198195-A.
                                                                   28-NOV-1990;
                                                                                                    28-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP05213769-A
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                                    17-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins having anticoagulant and antiinflammatory activity .
isolated from biological fluid by anion-exchange chromatographoc media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                 indicating that PAP-I is probably not constitutively secreted.

The Met residue is removed at in a post-translational event and the newly formed NH2-terminal Ala residue is blocked by acetylation. It binds to phospholipid and inhibits phopholipase A2.

The protein can substitute heparin or other anticosqulants in the treatment of disseminated intravascular coagulation, deep vein thrombosis, or other disorders. It also has antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CPB-I; stabilisation; frozen; molten; processed; activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.8%; Score 1586; DB 9;
99.4%; Pred. No. 8.5e-138;
11ve 0; Mismatches 2;
                                                                                                                                                                                                                                                                The protein does not contain a leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                    Carter BLA;
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                                                                                                                                                                                                                                    Disclosure; Page ?; ?pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR26276 standard; protein; 319
87US-0011782
87US-0059355
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 99.4
Matches 318; Conservative
                                                (ZYMO ) ZYMOGENETICS INC. (UNIW ) UNIV WASHINGTON.
                                                                                                    Fujikawa K, Irani MH,
                                                                                                                                 WPI; 1988-235049/33.
N-PSDB; AAN82107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 AA;
06-FEB-1987;
05-JUN-1987;
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04-FEB-1993
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26-FEB-2001; 2001JP-0050297
                                             Naruse H,
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                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                              AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV 248
                                                                                                                                                                                                                                                                         69 GRDLLDDLKSELTGRFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
                                                                                                                                                                                                                                                9 AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAOROEISAAFKTLF
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
calcium/phospholipid binding protein; polyhydric alcohol.
                                                                                                                                                                  Intravenously, orally, intramuscularly, percutaneously or rectally
                                                                                                                               Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I) inhibits protein kinase C (PKC) and is useful in the treatment of mailgnant tumours caused by abnormal activation of PKC. CPB-I is extracted from human or animal organs and may be applied
                                                                                    Protein kinase C inhibitor effective against malignant tumours contg. (opt. recombinant) calphobindin I
                                                                                                                                                                                                    Score 1585; DB 14; Length 319;
Pred. No. 1e-137;
0; Mismatches 1; Indels 0
                                           KOWA CO LTD.
ZH KAGAKU OYOBI KESSEN RYOHO KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 2-3; 6pp; Japanese
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                          92JP-0019032
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Matches 318; Conservative
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                                                                   WPI; 1993-299558/38
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                                           (KOWA ) KOWA
(KAGA-) ZH KA
         04-FEB-1992;
                         04-FEB-1992;
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                                                                                                                                                                                                                                                                                   The invention relates to eye drops contain CPB-I (anexin V) and a polyhydric alcohol having a carbonyl value of not more than 5micro Mol./g. The eyes drops are for treating e.g. corneal diseases. Such eye drops are without unpleasant irritation upon dropping but with satisfactory long-term storage stability. The present sequence is the human CPB-I (calcium/phospholipid binding) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSKSNAQRQEISAAFKTLF
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                                                                                                                                                 Eye drops for treating e.g. corneal diseases, contain CPB-I and polyhydric alcohol with specific carbonyl value, without unpleasant irritation upon dropping but with satisfactory long-term storability
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Pred. No. 1e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                              Inagi T;
(KOWA ) KOWA CO LTD.
(KAGA ) CHEMO-SERO-THERAPEUTIC RES INST
                                                                                                                                                                                                                                            Disclosure; Page 13-14; 16pp; Japanese
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Best Local Similarity 99.7
Matches 318; Conservative
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Sequence

Sequence 26476, A Appli Sequence 4, Appli Sequence 14, Appli Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 29, Appl Sequence 21, Appl Sequence 10, Appl

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US-09-234-245-2
US-08-955-762-14
US-09-911-927-14
US-09-911-88-14
US-09-911-156A-21
US-09-011-156A-21
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Description	Sequence 2, Appli	9	4	ω,	7	Patent No. 5225537	Sequence 1, Appli	7	'n	7	4	Sequence 14, Appl	'n	4	'n	Sequence 13, Appl	ý	62,	65,	99	4, 4	63,	Sequence 64, Appl	7,7	~	Sequence 2, Appli	9
ID	US-09-324-096A-2	US-09-324-096A-6	US-09-324-096A-4	US-08-125-746-3	US-08-948-276-1	5225537-4	US-08-125-746-1	US-08-948-276-2	US-08-948-276-3	US-08-149-975A-2	US-08-948-276-4	US-08-526-136-14	US-08-526-136-2	US-08-526-136-4	US-08-948-276-5	US-08-526-136-13	US-08-948-276-6	US-09-325-932A-62	US-09-325-932A-65	US-09-325-932A-66	US-09-157-257-4	US-09-325-932A-63	US-09-325-932A-64	US-08-923-511-2	US-09-416-874A-2	US-09-603-185-2	US-09-157-257-6
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	SULT 1 -09-324-096A-2 Sequence 2, Application US/09324096A Betten No. 632313 GENERAL INFORMATION: APPLICANT: Talt, Jonathan APPLICANT: Brown, David TITLE OF INVENTION: ANNEXIN DERIVATIVE WITTLE PETERENCE: UOFW-1-1344 CURRENT APPLICATION NUMBER: US/09/324,096A CURRENT APPLICATION NUMBER: US/09/324,096A CURRENT FILING DATE: 1999-06-01 NUMBER OF SEQ ID NOS: 12 SOFTWARE: PATENTIN VERSION 3.0 LENGTH: 327 TYPE: PRT ORGANISM: HOMO Sapiens -09-324-096A-2	Query Match Best Local Similarity Matches 327; Conser		61	121 121	181 181	241	301
	SULT 1 -09-324-096 Satetine 2, Satetine 3, Satetine 3, APPLICANT: TITLE OF I	Query Match Best Local Matches 32						
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SUMMARIES

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                       GENERAL INFORMATION:
APPLICANT: Tait, Jonathan
APPLICANT: Tait, Jonathan
APPLICANT: Tait, Jonathan
APPLICANT: Brown, David
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES
FILE REFERENCE: UOFW-1-13841
CURRENT APPLICATION NUMBER: US/09/324,096A
CURRENT FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.0
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Sequence 4, Application US/09324096A

GENERAL INFORMATION

APPLICANT: Tait, Jonathan

APPLICANT: Brown, David

ITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES

FILE REPERENCE: US/09/324,096A

CURRENT APPLICATION NUMBER: US/09/324,096A

CURRENT FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.0
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Pred. No. 1.3e-149;
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Pred. No. 1.9e-148;
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Sequence 6, Application US/09324096A
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Best Local Similarity 99.4%;
Matches 325; Conservative (
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Best Local Similarity 99.7
Matches 326; Conservative
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo saptens
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                                                                                                                                                                 SEQ ID NO 6
LENGTH: 327
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121 IASRTPEELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVE 180
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                                                                                                                                                                                                                                                                                         EQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFA 300
                                                                                                                                                                                            ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SAINO, YUSHI
APPLICANT: IMASAKI, AKIO
APPLICANT: SUDA, MAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
CORRESPONDENCE: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-FEB 1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 184428/1987
FILING DATE: 23-JUL-1987
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5591633man F.
REGISTRATION NUMBER: 24.618
REFERENCE/DOCKET NUMBER: 80-074-0 DIV
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           301 TSLYSMIKGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 037227/1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
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PHOSPHOLIPID-BINDING PROTEINS
NUMBER OF SEQUENCES: 14
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/459,082
FILING DATE: 29-DEC-1989
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APPLICATION UNMBER: US/08/125,746
FILING DATE: 24-SEP-1993
CLASSIFICATION: 530
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   301 KGDTSGDYKKALLLLCGEDD 320
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COMPUTER READABLE FORM:
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Best Local Similarity
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   Length 320;
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 Score 1590; DB 1;
Pred. No. 9.5e-146;
0; Mismatches 1;
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Pred. No. 9.5e-146;
0; Mismatches 1;
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APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UGSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PAtentin Ver. 2.0
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il Similarity 99.7%;
319; Conservative
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Best Local Similarity 99.7%;
Matches 319; Conservative
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US-08-948-276-1
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  Query Match
Best Local 9
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1755 S. Jefferson Davis Highway, Suite 400
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SAINO, YUSHI
APPLICANT: TWASAKI, AKIO
APPLICANT: SUDA, WAKOTO
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: P.C.
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APPLICANT: FOSTER, DONALD TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID
                                                                                                                                                                                                             Score 1590; DB 6;
Pred. No. 9.5e-146;
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                      1; Gaps
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                      Indels
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88.8%; Score 1455.5; DB 4;
Best Local Similarity 91.8%; Pred. No. 9.6e-133;
Matches 291; Conservative 12; Mismatches 13;
         Pred. No. 4.6e-135
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APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSP97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                     9; Mismatches
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Patent No. 6511829
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                   Conservative
      Best Local Similarity
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; ORGANISM: rat
US-08-948-276-3
                   296;
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                                                                                                                                                                                                                                                                                                                                                                            Length 319;
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                                                                                                                                                                                                                                                                                                                                                                         Score 1585; DB 1;
Pred. No. 2.9e-145;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
URMBER OF SEQ ID NOS: 6
SOFWARE: Patentin Ver. 2.0
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/807,623
FILING DATE: 13-DEC-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 037227/1987
FILING DATE: 20-PEB-1987
FILING DATE: 20-PEB-1987
FILING DATE: 20-UL-1987
ATORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: UP 184428/1987
FILING DATE: 23-UL-1987
ATORNEY/AGENT INFORMATION:

REFERENCE/COCKET NUMBER: 80-074-0 DIV
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-2220
TELEFAK: (703) 413-2220
TELEFAK: (703) 413-2220
TELEFAK: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.3%; Score 1479.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDTSGDYKKALLLCGEDD 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                       tch 96.7%;
al Similarity 99.7%;
318; Conservative
                                                                                                                                                                                                                                                                                   : 319 amino acids amino acids
                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-125-746-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: mouse
                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-948-276-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 319
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                                                                                                                                                                                                                                                                                                                                                                                        Local
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74 DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 313
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                                                                                                                                                                                                                                                                                                                                            Ouery Match 56.3%; Score 923; DB 4; Length 321; Best Local Similarity 58.3%; Pred. No. 3.2e-81; Matches 183; Conservative 53; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                             APPLICANT: Ernst, Joel D.
TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSP97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEO ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:
APPLICANT: Towle, Christine A. et a
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            et
                     Sequence 4, Application US/08948276
Patent No. 6511829
GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                   ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
US-08-526-136-14
                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 321
      JS-08-948-276-4
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                             Sequence 2. Application US/08149975A

Patent No. 5849600
GENERAL INFORMATION:
APPLICANT: Naton, Ralph
APPLICANT: Honda, Toshlyuki
TITLE OF INVENTION: DIAGNOSTIC ASSAVS FOR ALZHEIMER'S
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: O2110-2804
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC Compatible
COMPUTER: BM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
CORPUTER: Patentin Release #1.0, O2184
COMPUTER: Patentin Release #1.0, O2184
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Best Local Similarity 91.5%; Pred. No. 4.6e-132;
Matches 290; Conservative 12; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04843/016001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-9906
TELEFAX: 617/542-9906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/149,975A FILING DATE: 11-NOV-1993 CLASSIFICATION: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: no
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RESULT 10
US-08-149-975A-2
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CLASSIPCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE: PEBruary 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: FEBruary 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08526136
Patent No. 6107089
GENERAL INFORMATION:
APPLICANT: TOWIE, Christine A. et
TITLE OF INVENTION: ANNEXIN XI
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||:| || : | :|
|GDYRKILLKICGGND 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 54.9%
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                             TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 225 Franklin
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: N/A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 IPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 GTVKAASGFNAAEDAQTLRKAMKGLGTDEDAIINVLAYRSTAQRQEIRTAYKTTIGRDLM 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 55.8%; Score 914; DB 3; Length 319; Best Local Similarity 58.0%; Pred. No. 2.3e-80; Matches 182; Conservative 51; Mismatches 81; Indels
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COMPUTER READABLE FORM:
MEDUUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATIG SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
    AFLIANCE DATE:
PILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/64,465
FILING DATE: September 23, 1991
ATORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 0786/099001
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 542-5070
TELEFAX: (617) 542-8906
TELEFAX: (617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/214,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/526,136
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Sequence 2, Application US/08526136

Patent No. 6107089

GENERAL INFORMATION:

APPLICANT: TOWIC, Christine A. et

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:| ||:| | || || DYRKVLLILCGGDD 319
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                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massach
COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-526-136-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
                                                                                                                                                                                                     193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
                                                                                                                                                                                                                                                                                                                                                                                         133 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL 72
                                               Gaps
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
52.8%; Score 865; DB 3; 54.9%; Pred. No. 2.5e-75; tive 58; Mismatches 84;
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TITLE OF INVENTION: GFP-Annexin Fusion Proteins
FILE REFERENCE: UCSF97-113
CURRENT APPLICATION NUMBER: US/08/948,276
CURRENT FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                              00786/099001
              APPLICATION NUMBER: US/08/526,136 FILING DATE:
                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
                                                                                                                                    FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNATION INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                     07/837,775
                                                                                                                                                                                                                                            TELECHAUNICATION INFORMATION:
TELECHAUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-6906
. TELEFAX: 200154
. INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08948276
Patent No. 6511829
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Best Local Similarity 54.9
Matches 173; Conservative
CURRENT APPLICATION DATA:
                                                                                                    FILING DATE:
APPLICATION NUMBER:
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; ORGANISM: human
US-08-948-276-5
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                                                                                                                                                                                  122 SROMKDISQAYYTVYKKSLGDDISSETSGDFRKALLTLADGRRDESLKVDEHLAKQDAQI 181
                                                                                                                                                                                                                                                                   246 AVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYS 305
                                                                                                                                                                                                                                                                                  61
                                                                                                                      6 GHMAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFK
                                                                  66 TLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRT
                                                                                                                                                                                                              186 LFQAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLL
                           Gaps
                          5
 Length 323
49.0%; Score 802.5; DB 4; 49.4%; Pred. No. 1.5e-69;
                          61; Mismatches
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             Similarity
Query Match
Best Local Simi
Matches 159;
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Search completed: August 22, 2003, 21:37:04 Job time : 20.3333 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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 protein search, using sw model OM protein Run on:

August 22, 2003, 21:30:17; Search time 15 Seconds (without alignments) 2096.477 Million cell updates/sec

US-09-970-969-2 1639 Title: Perfect score: Sequence:

1 MACGGGHMAQVLRGTVTDFP......KGDTSGDYKKALLLLSGEDD 327

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITMMARTEC

	Description	annexin V (validat	>	, >	annexin V - chicke	annexin VI [valida	annexin VI - mouse	annexin IV - human	annexin IV - pig	annexin VI - rat	annexin IV - bovin	annexin - chicken	annexin XI form A	annexin XI form B	annexin XI - rabbi	annexin XI - human	н	annexin III - huma	Γ,	annexin III - rat	annexin VII - mous	٠	ı	hypothetical prote		annexin II - bovin	annexin II - rat	annexin II - mouse	annexin II - rat	annexin IX - fruit
SUMMARIES	а	AOHUP	S27214	LURT5	LUCHS	AQHU68	S01786	A42077	LUPG4	S52844	LUBO4	JC2029	LUBO11	S23447	LURB11	· A53152	LUHUB	LUHU3	LUHU7	LURT3	S29170	LUJF12	S70644	S41022	LUHU36	LUBO36	833700	LUMS36	S55277	LUFF9
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	Query Match Length DB	320	320	319	321	673	673	321	318	673	319	671	503	505	503	505	327	323	488	324	463	316	512	9/9	339	339	339	339	341	296
ď	Query Match	97.0	93.7	88.8		3	56.9	56.3	56.2	56.2		54.	52.					49.0	47.5	47.3	47.2	43.8	43.4	43.3	42.6	42.4	42.3	42.3	41.6	41.6
	Score	1590	1536.5	1455.5	1279	932	932	923	921	921	914	896.5	865	865	863	855	831.5	802.5	779	775	773	718	711	709	698.5	694.5	693.5	691.5	682.5	682
	Result No.	-	7	e	4	ĸΩ	w	7	æ	σ	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	53

A; Cross-Teferences: EMBL:M18366; NID:g179131; PIDN:AAA35570.1; PID:g179132
A;Cross-Teferences: EMBL:Makao, H.; Nagoya, T.; Saino, Y.; Arai, K.; Mizoguchi, T.; S
J; Wassaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saino, Y.; Arai, K.; Mizoguchi, T.; S
J. Biochem. 102, 1261-1273, 1987
A;Title: Structure and expression of cDNA for an inhibitor of blood coagulation isola

A; Molecule type: mRNA A; Residues: 1-320 <FUN>

A; Molecule type: mRNA
A; Residues: 1-320 <MAU>
A; Residues: 1-320 <MAU>
A; Cross-references: EMBL:X12454; NID:g37636; PIDN:CAA30985.1; PID:g37637
A; Note: part of this sequence was confirmed by protein sequencing
A; Note: part of this sequence was confirmed by protein sequencing
B; Funakoshi, T.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
Biochemistry 26, 8087-8092, 1987
A; Title: Primary structure of human placental anticoagulant protein.
A; Reference number: A29417; MUID:88163463; PMID:2964863
A; Accession: A29417

,,,,,,		annexin I · guinea annexin I · human annexin I · bovine annexin I · rat annexin I · rat	
LUHUIS JO1298 LUFF10	J01297 A57076 B57076 LUCH2	LUGP1 LUHU S28228 LURT1 A44118	LUMS1 E88452 LUPY1 LUJP1
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316 340 321	340 316 357 339	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	346 322 341 346
41.4 41.4 11.4	41.2 40.9 40.9	38 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	38.1 35.5 33.3
679 678.5 678	675.5 671 671 666.5	648 643 632 630	624 582 578.5 542
30 31 32		338 338 40 41	4 4 4 4 2 6 4 3 5

ALIGNMENTS

	RESULT 1 AQHUP
	annexin V [validated] - human N;Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; place C:Sneries: Homo sanions (man)
	C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000 C:Accession: D20250: A30206: A28076: S01016: A28417: A41514: A28038: C31953: S06646:
	R; Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Brownin J Biol Chem 263 10700-10811 1088
	A; Title: Five distinct calcium and phospholipid binding proteins share homology with
	A; Neterence immuder: Azzosy; MolD:002/3201; FMID:200903 A; Accession: D20220
	A; Molecule type: mRNA
_	A) Residues: 1-320 < PEP)
	A;Cross_reperences; GB:MAI/13; NID:1918095; PIDN:AAA301001; PID:1930/LIO B:Arundmann II ahal K I ahah H - Loabarmann H - Lottenaich F - Kupner H
	Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988
	A, Title: Characterization of cDNA encoding human placental anticoagulant protein (PP4
_	A; Reference number: A30206; MUID:88234495; PMID:2967495
_	A; Accession: A30206
_	A; Molecule type: mRNA
_	A; Residues: 1-320 <gru></gru>
_	A;Cross-references: GB:M19384; NID:g189614; PIDN:AAB59545.1; PID:g189615
_	R; Kaplan, R.; Jaye, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.
_	J. Biol. Chem. 263, 8037-8043, 1988
_	A; Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+) and phosphol
_	A; Reference number: A28076; MUID:88228020; PMID:2967291
_	A; Accession: A28076
_	A; Molecule type: mRNA
	A; Residues: 1-320 < KAP>
_	A; Cross-references: GB: J03745; NID: 9182111; PIDN: AAA52386.1; PID: 9182112
	R; Maurer-Fogy, I.; Reutelingsperger, C.P.M.; Pieters, J.; Bodo, G.; Stratowa, C.; Hau
_	Eur. J. Biochem. 174, 585-592, 1988
_	A; Title: Cloning and expression of cDNA for human vascular anticoagulant, a Ca-depend
_	A; Reference number: S01016; MUID:88271329; PMID:2455636
_	A; Accession: S01016
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Gaps ö

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A; Residues: 1-320 <LEA>
A; Residues: 1-320 <LEA>
A; Residues: 1-35, T', 37-124, E', 126-320 <LE2>
A; Residues: 1-35, T', 37-124, E', 126-320 <LE2>
A; Residues: It is uncertain whether the sequence differences are due to allelic variation C; Comment: Annexins undergo reversible, calcium-dependent binding to membrane phosphoderstood.
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N.Alternate names: CaBB33; CaBB37
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jun-1994 **sequence_revision 10-Feb-1995 **text_change 26-Feb-1999
C;Accession: S27214; S27215
R;Learmonth, M.P.; Howell, S.A.; Harris, A.C.M.; Amess, B.; Patel, Y.; Glambanco, I.; Biochim. Biophys. Acta 1160, 76-83, 1992
A;Title: Novel isoforms of CaBP 33/37 (Annexin V) from mammalian brain: structural an A;Reference number: S27214; MUID:93041974; PMID:1420335
F;33,35,36/Binding site: calclum, low affinity (Thr, Glu, Glu) *status experimental F;737,8/Binding site: calclum, low affinity (Leu, Glu) *status experimental E:100,102,104,4/Binding site: calclum, high affinity (Leu, Gly, Gly, Asp) *status F;259,261,663,303/Binding site: calclum, high affinity (Met, Gly, Asp) *status
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                                                                                                                                                                                                                                                Score 1590; DB 1; Length 320;
Pred. No. 8.6e-95;
0; Mismatches 1; Indels
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Best Local Similarity 99.7%;
Matches 319; Conservative (
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A: Introns: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
C: Superfamily: annexin repeat homology
C: Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin F; 2-320/Product: annexin repeat homology <AXI>F: 29-45/Region: endonexin fold *status predicted
F: 99-45/Region: endonexin fold *status predicted
F: 90-161/Domain: annexin repeat homology <AXI>F: 10-111/Region: endonexin fold *status predicted
F: 90-150/Domain: annexin repeat homology <AXI>F: 185-201/Region: endonexin fold *status predicted
F: 249-320/Domain: annexin repeat homology <AXI>F: 185-201/Region: endonexin fold *status predicted
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F: 249-320/Domain: annexin fold *status predicted
F: 249-320/Domain: annexin fold *status predicted
F: 249-320/Domain: annexin fold *status predicted
F: 249-320/Domain: annexin fold *status delicted
F: 249-320/Domain: annexin fold *status delicted
F: 249-320/Domain: annexin fold *status delicted
F: 249-320/Domain: annexin fold *status predicted
F: 249-320/Domain: annexin fold *status predicted
F: 249-320/Domain: annexin fold *status delicted
F: 240-140/Bodomain delicted annexin fold *status delicted
F: 240-140/Bodomain delicted annexin fold *status delicted
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A; Molecule type: protein
A; Residues: 85-93 (ANN)
R; Rothhut, B.; Comera, C.; Cortial, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; Cc
Biochem. J. 263, 929-935, 1989
Ashorhem. A. 28 kDa lipocortin from human mononuclear cells appears to be identical with the A; Reference number: S06646; MUID:90088443; PMID:2532007
                                                                                                  A; Molecule type: mRNA
A; Residues: 1-320 < IMA
A; Residues: 1-320 < IMA
A; Cross-references: GB: D00172; NID: g219480; PIDN: BAA00122.1; PID: g219481
A; Note: part of this sequence was confirmed by protein sequencing
R; Schlaepfer, D.D.; Mehlman, T.; Burgess, W.H.; Haigler, H.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987
A; Title: Structural and functional characterization of endonexin II, a calcium- and phos
A; Reference number: A28038; MUID: 87317598; PMID: 2957692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A. Molecule type: protein

A. Molecule type: protein

A. Mayr, 15-11;181-198;202-207;209-226;228-238;246-271;277-282;

R. Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.

R. Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.

R. Efter. 275, 15-21, 1990

A. Title: The calcium binding sites in human annexin V by crystal structure analysis at 2 A: Reference number: A3750; MUID:91085549; PMID:2148156

A. Contents: annotation; X-ray crystallography, 2.0 angstroms

A. Note: three calcium ions are strongly bound at sites in the first, second, and fourth Biochemistry 26, 5572-5578, 1987

A. Title: Human placental anticoagulant protein: isolation and characterization.

A. Reference number: A29670; MUID:88050845; PMID:2960376
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A;Cross-references: EMBL:U01691; NID:9430964; PIDN:AAB40047.1; PID:9430966
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
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A; Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>
A; Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>
B; Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
J. Biol. Chem. 263, 18657-18663, 1988
A; Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-
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Gene 149, 253-260, 1994
A;Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C
A;Reference number: I37172; MUID:95047484; PMID:7958998
     A; Reference number: A41514; MUID:88139278; PMID:2963810
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A;Molecule type: DNA
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A;Residues: 29-73;274-297;300-320 <FU2>
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C;Genetics:
A;Introns: 1/3; 30/1; 61/3; 99/3; 130/1; 156/3; 175/3; 207/1; 239/1; 258/3; 299/3
C;Superfamily: annexin I; annexin repeat homology
C;Keywords: calcium binding; duplication; endonexin fold; membrane-associated protein; proceed; scalcium binding; duplication; endonexin fold #status predicted
F;16-87/Domain: annexin repeat homology <AXI>
F;18-115/Pomain: annexin repeat homology <AXI>
F;18-115/Pomain: annexin repeat homology <AXI>
F;181-15/Pomain: annexin repeat homology <AXI>
F;181-19/Pomain: annexin repeat homology <AXI>
F;181-19/Pomain: annexin repeat homology <AXI
F;28-274/Region: endonexin fold #status predicted
F;26,28,30,70/Binding site: calcium, high affinity (Met, Glu, Asp) #status predicted
F;31,33,34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nalternate names: endonexin II; lipocortin V; placental anticoagulant protein; placental (Species: Rattus norvegicus (Norway rat) (C;Species: Rattus norvegicus (Norway rat) (C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999 (C;Accession: C29250; S6680 (Species: R;Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning, A;Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning, A;Tile: Five distinct calcium and phospholipid binding proteins share homology with lift A;Reference number: A92659; MUID:88273202; PMID:2968983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rimal, Y.; Kohaaka, S.
Bur. J. Blochem. 232, 327-334, 1995
Aritle: Structure of rat annexin V gene and molecular diversity of its transcripts. A; Reference number: $66680; MUID:96035863; PMID:7556178
A; Reference number: $66680
A; Status: preliminary: translation not shown
A; Molecule type: DNA
A; Residues: 1-319 < IRMA
A; Residues: 1-319 < IRMA
A; Residues: Linka
A; Cross-references: EMBL:042136
C; Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholif
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                                                                                                                                                                                                                                                                                                   LRAIKOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ 188
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                                                      Gaps
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A;Residues: 1-319 <PEP>
A;Cross-references: GB:M21730; NID:9205138; PIDN:AAA41512.1; PID:9205139
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Length 320;
                                                   Indels
Score 1536.5; DB 1;
Pred. No. 2.3e-91;
5; Mismatches 5;
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93.78;
                       al Similarity 96.6
309; Conservative
Query Match
Best Local S
Matches 309
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A; Molecule type: mRNA
A; Cross references: 1-118, 'LLKCRILNRFNMQEYEANLGRNKITGRRHQAIFRDCWMSCCRQIEI', 163-167, 'E', 169-32
A; Cross references: GB: M30971; GB: J03194; NID: 91211138
B; Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthier, R.E.
J. Biol. Chem. 266, 10678-10685, 1991
A; Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective parti
A; Reference number: A40404; MUID: 91244852; PMID: 2037607
F;71,76/Binding site: calcium, low affinity (Leu, Glu) #status predicted F;98,100,102,142/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp) #status pr F;257,259,261,301/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status p
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A; Molecule type: mRNA
A; Residues: 1-321 < FERA
A; Residues: 1-321 < FERA
A; Cross-references: GB:M30971; GB:J03194; NID:g211138; PIDN:AAA48591.1; PID:g211139
A; Cross-references: GB:M30971; GB:J03194; NID:g211138; PIDN:AAA48591.1; PID:g211139
B; Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R.;
J. Biol. Chem. 263, 35921-5925, 1988
A; Reference number: A28623; MUID:88186917; PMID:2833522
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A;Molecule type: profesor
A;Residues (520;85, X',87-88, X',90-93, X',95-96,'XX',99-100,'X',102-103,'XX',106-10
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho
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Blochem, J. 291, 601-608, 1993
A;Title: Isolation, characterization and localization of annexin V from chicken liver
A;Reference number: 332523; MUID:93249384; PMID:8484740
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C; Species: Gallus gallus (chicken)
C; Species: 30-899-1992 #sequence_revision 20-597-1850-1992 #text_change 02-Jun-2000
C; Accession: A35381; A28623; B40404; S2352-35; S08771
R; Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R.; J. Biol. Chem. 265, 8344, 1990
A; Reference numbor: A35381; MUID:90243721; PMID:2159478
A; Contents: erratum
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                                                                                                                                Length 319;
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                                                                                                                                   DB 1;
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                                                                                                                            88.8%; Score 1455.5; DB 3 91.8%; Pred. No. 3.6e-86; tive 12; Mismatches 13
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    chicken

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13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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52; Mismatches
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Best Local Similarity 58.1%
Matches 183; Conservative
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:254-325/Domain:
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C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
C;Date: 31-Mar-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
C;Accession: JU0032; S00263; S18519; A31079; JX0091; B34459; B31953; A53507
R;Iwasaki, A: Suda, M:; Matanabe, M:; Nakao, H:; Hattori, Y:; Nagoya, T:; Saino, Y:; Sh J: Blochem. 106, 43-49, 1989
A;Title: Structure and expression of cDNA for calphobindin II, a human placental coagula A;Reference number: JU0032; MUID:89380132; PMID:2528841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p68
A;Reference number: S00263; MUID:88196081; PMID:3258820
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A;Residues: 1-673 cTWA>
A;Residues: 1-673 cTWA>
A;Cross-references: EMBL:D00510; NID:g219550; PIDN:BAA00400.1; PID:g219551
A;Crompton, M.R.: Ovens, R.J.: Totty, N.F.; Moss, S.E.; Waterfield, M.D.; Crumpton, EMBO J. 7, 21-27, 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annexin VI [validated] - human
N;Alternate names: calcium-binding protein, 68K; calelectrin; calphobindin II
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A;Cross-references: EMBL:Y00097; NID:g35217; PIDN:CAA68286.1; PID:g35218
A;Accession: S18519
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                                                                                                                                                                                                                                                                                                                                                                            Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
                                                                                                                                                                                                                                                                                                                                                                          Query Match
78.0%; Score 1279; DB 1;
Best Local Similarity 78.1%; Pred. No. 7.3e-75;
Matches 250; Conservative 38; Mismatches 32;
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A. Residues: 103-113;167-172, 'X', 174-177;232-235,'F',237-240;251-258;277-281;359-362,'A;Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-A;Note: eight calcium ions are bound in the presence of phospholipid Bysuedhof, T.C.; Slaughter, C.A.; Leznicki, I.; Barjon, P.; Reynolds, G.A. Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988
A;Titles Human 67-kDa calelectrin contains a duplication of four repeats found in 35-A;Accession: A31079; MUID:88124902; PMID:2963335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 2-299;307-314;320-445;447-549;581-673 <YOS>
A;Residues: 2-299;307-314;320-445;447-549;581-673 <YOS>
B;Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga, T.
Biol. Chem. 264, 1722-17230, 1989
A;Itile: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding prot A;Reference number: A34459; MUID:900008800; PMID:2529258
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A; Residues: 90-108, 'L', 110-126,127, 265-276,286-302; 626-654 <AHN>
A; Residues: 90-108, 'L', 110-126,127, 265-276,286-302; 626-654 <AHN>
R; Hyatt, S.L.; Liao, L.; Chapline, C.; Jaken, S.
Biochemistry 33, 122-1228, 1994
A; Title: Identification and characterization of alpha-protein kinase C binding protein
A; Reference number: A53507; MUID:94153907; PMID:8110754
A; Accession: A53507
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A;Map position: 5432-5434
C;Superfamily: annexin VI; annexin repeat homology
C;Superfamily: annexin VI; annexin repeat homology
C;Stywords: accetylated amino end; calcium binding; duplication; endonexin fold; phosp
F;2-673/Product: annexin VI #status experimental <MAT>
F;23-94/Domain: annexin repeat homology <AXI>
F;34-50/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 10-25:69-75;136-151;192-207;209-220;300-306 <HAY>
A; Residues: 10-25:69-75;136-151;192-207;209-220;300-306 <HAY>
A; Experimental source: placenta
B; Ahn, N.G.; Teller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C
J. Blol. Chem. 263, 18657-18663, 1988
A; Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Structure and properties of calphobindin II, an anticoagulant protein from A; Reference number: JX0091; MUID:90236978; PMID:2139657
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                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-225, MK', 228-554, T',556-673 <SUE>
A; Cross-references: GB:J03578; NID:g179975; PIDN:AAA35656.1; PID:g179976
A; Toshizaki. H; Mizoguchi, T.; Arai, K.; Shiratsuchi, M.; Shidara, Y.; Maki,
J. Blochem. 107, 43-50, 1990
A; Title: Structure and properties of calphobindin II: an anticoagulant protein
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A;Residues: 'X',473-480,'DY' <HYA>
C;Comment: This abundant cytosolic protein binds to the inner surface of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 673
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Pred. No. 3.1e-52;
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F;106-122.Region: endonexin fold #status predicted
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#status predicted
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F:613-629/Region: endonexin fold #status predicted
F:2/Modified site: acetylated amino end (Ala) (in
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A; Residues: 29-58; 01-126; 282-310 < AHN>
A; Residues: 29-58; 01-126; 282-310 < AHN>
R; Talt, J.F.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E Biochemistry 27, 6268-6276, 1988
A; Title: Placental anticoagulant proteins: isolation and comparative characterization A; Reference number: A90534; MUID:89118212; PMID:2975506
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C;Species: Homo sapiens (man)
C;Date: 30-Jan-1993 *sequence_revision 26-May-1994 *text_change 22-Jun-1999
C;Accession: A42077; B42077; S07434; A31953; A31046
C;Accession: A42077; B42077; S07434; D.A.; Miao, C.H.; Adler, D.A.; Disteche, Genomics 12, 313-318, 1992
A;Title: Circmosomal mapping of the human annexin IV (ANX4) gene.
A;Reference number: A42077; MUID:92155721; PMID:1346776
A;Accession: A42077
                                                                                                                                                                                                     252
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                                                                                                                                                                                                                                                                                                                                                                                                          SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                              133 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                         KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
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F;30-46/Region: endonexin fold #status predicted
F;91-162/Domain: annexin repeat homology <AX2>
F;102-118/Region: endonexin fold #status predicted
F;174-246/Domain: annexin repeat homology <AX3>
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A; Residues: 4-17;30-74;102-146;283-321 <TA3>
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A; Introns: 102/3
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A; Residues: 1-321 <TAI>
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NiAlterante names: calcium-binding protein p68; calelectrin; calphobindin II

C;Species; Mus musculus (house mouse)

C;Date: 30-Sep-1889 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C;Accession: S01786

R;Moss, S.E.; Crompton, M.R.; Crumpton, M.J.

Bur. J. Blochem. 177, 21-77, 1988

A;Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family.

A;Reference number: S01786; MUID:89030687; PMID:2972541

A;Residues: 1-673 - MOSS

A;Residues: 1-673 - MOSS

A;Residues: 1-673 - MOSS

A;Cross-references: EMBL:X13460; NID:953580; PIDN:CAA31808.1; PID:953581

A;Note: the authors translated the codon GCC for residue 329 as Gly

C;Comment: This sbundant cytosolic protein binds to the inner surface of the cell membra
C;Superfamily: annexin VI; annexin repeat homology AXI>

F;24-50/Apcalon: annexin repeat homology AXI>

F;34-50/Apcalon: annexin repeat homology AXI>

F;34-50/Apcalon: annexin repeat homology AXI>

F;106-122/Region: endonexin fold #status predicted
F;25-32/Apcmain: annexin repeat homology AXI>
F;106-122/Region: endonexin fold #status predicted
F;26-32/Apcmain: annexin repeat homology AXI>
F;26-32/Apcmain: annexin repeat homology AXI
F;27-33/Apcmain: annexin repeat homology AXI
F;27-34/Apcmain: annexin repeat homology AXI

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F;613-629/Region: endonexin fold *status predicted
F;2/Modified site: acetylated amino end (Ala) (in mature form) *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 KOVYEBEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
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RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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F;449-465/Region: endonexin fold *status predict
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Best Local Similarity 59.09
Matches 186; Conservative
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C.Species: Rattus norvegicus (Norway rat)

C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C.Accession: S65683; S52844

R.Fan, H.; Josic, D.; Lim, Y.P.; Reutter, W.

Eur. J. Blochem. 230, 741-751, 1995

A.Title: cDNA cloning and tissue-specific regulation of expression of rat calcium-bin

A.Reference number: 865683; MUID:95331313; PMID:7607247
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          64
              GTVKAASGFNAAEDAQTLRKAMKGLGTDEDAIISVLAYRSTAQRQEIRTAYKSTIGRDLL
                                                                             DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK
                                                                                                                                                                                                                  QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
                                                                                                                                                                                                                                                                                                                                                       WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
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A,Residues: 1-673 <PAN>
A,Cross-references: EMBL:X86086; NID:g763180; PIDN:CAA60040.1; PID:g763181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A) Experimental source: liver
C; Superfamily: annexin VI; annexin repeat homology
C; Keywords: acetylated amino end; calcium binding;
E; 2-673 Product: annexin VI #status predicted <AMT>
F; 23 94 Domain: annexin repeat homology <AXI>
F; 95 -166 Domain: annexin repeat homology <AXI>
F; 95 -166 Domain: annexin repeat homology <AXI
F; 95 -166 Domain: annexin repeat homology <AXI
F; 95 -166 Domain: annexin repeat homology <AXI
F; 106 -122 Region: endonexin fold #status predicted
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annexin repeat homology <AX4>
endonexin fold *status predicted
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#status predicted
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DYRKVLLILCGGDD 318
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C; Superfamily: annexin I; annexin repeat homology
C; Superfamily: annexin repeat homology < AXI>
F; 16-87/Domain: annexin repeat homology < AXI>
F; 27-43/Region: endonexin fold #status predicted
F; 88-115/Region: endonexin fold #status predicted
F; 99-115/Region: endonexin repeat homology < AXI>
F; 19-115/Region: endonexin fold #status predicted
F; 247-318/Domain: annexin repeat homology < AXI>
F; 18-13-139/Region: endonexin fold #status predicted
F; 247-318/Domain: endonexin fold #status predicted
F; 1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental
F; 6/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F; 124, 244/Binding site: carbohydrate (Asn) (covalent) #status predicted
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(C.Species: Sus scrofa domestic plg)
(C.Spate: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 24-Nov-1999
(C.Accession: A27107
(C
F;186-202/Region: endonexin fold #status predicted
F;250-321/Domain: annexin repeat homology <AX4>
F;251-277/Region: endonexin fold #status predicted
F;27/Nodified site: acetylated amino end (Ala) (in mature form) #status predicted
F;9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;247/Reinding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
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                                                                                                                                                                                                                                                                                                                                                                                                                       254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSĞ
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                                                                                                                                                                                                                                              56.3%; Score 923; DB 1; Length 321; 58.3%; Pred. No. 4.7e-52; Live 53; Mismatches 78; Indels
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Matches 184; Conservative
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Matches 183; Conserv
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67-kDa annexin from chicken
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: JC2029
A;Title: Characterization, cloning and expression of the 67-kDa annexin from chick A;Reference number: JC2029; MUID:94092130; PMID:8267590
A;Accession: JC2029
A;Molecule type: mRNA
A;Residues: 1-671 CCAO>
C;Superfamily: annexin repeat homology AXX>
C;Superfamily: annexin repeat homology AXX>
F;321-92/Domain: annexin repeat homology AXX>
F;325-323/Domain: annexin repeat homology AXX>
F;325-323/Domain: annexin repeat homology AXX>
F;325-333/Domain: annexin repeat homology AXX>
F;225-37/Domain: annexin repeat homology AXX>
F;225-37/Domain: annexin repeat homology AXX>
F;225-597/Domain: annexin repeat homology AXX>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKG 309
                                           DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
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                                                                                  WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                                                                                                                                                                                                                        QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
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A.Residues: 1-319 CHAM>
A.Roossidues: 1-319 CHAM>
A.Roossidues: 1-319 CHAM>
A.Roossidues: 1-319 CHAM>
A.Roossidues: 1-310 CHAM>
A.Roossidues: 1-310 CHAM>
A.Reference number: A45066; MUID:93015942; PMID:1400371
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A; Residues: 10-18, 'X', 20-22, 'X', 24-25, 29-48; 101-107, 'X', 109-118; 'X', 194-197, 'Y', 199, 'X',
A; Residues: 10-18, 'X', 20-22, 'X', 24-25, 29-48; 101-107, 'X', 109-118; 'X', 194-197, 'Y', 199, 'X',
A; Restidues: 10-18, 'X', 20-22, 'X', 24-25; 29-48; 101-107, 'X', 109-118; 'X', 194-197, 'Y', 199, 'X',
A; Note: squence extracted from NCBI backbone (NCBIP:116211, NCBIP:116208, NCBIP:116209,
A; Note: 12-Met and 12-Tyr were also found
A; Note: 12-Met and 12-Tyr were also found
A; Note: 12-Met and 12-Tyr were also found
A; Sohma, J; 312, 175-181, 1995
A; Title: Ca(2+)-dependent binding of annexin IV to surfactant protein A and lamellar bod
A; Reference number: S59624; MUID:96077142; PMID:7492310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAIternate names: 32K calelectrin; chromobindin IV; endonexin; lipocortin IV; protein I (Species: Bos primigenius taurus (cattle) (C.Species: Bos primigenius (C.Species: Bos primigenius (C.Species: Bos primigenius (C.Species: Bos primigenius (C.S. L.C.; Lynch, K.R.; Creutz, C.E. Bochen, Blophys. Res. Commun. 156, 660-667, 1988 (C.B. A;Itle: Cloning and characterization of a cDNA encoding bovine endonexin (chromobindin A;Reference number: A31578; MUID:89050088; PMID:2847715
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C:Reywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid PF:2-319/Product: annexin Iv $status predicted <WAT>
F:2-319/Product: annexin repeat homology <AXI>
F:28-44/Region: endonexin fold *status predicted
F:28-44/Region: endonexin fold *status predicted
F:30-116/Region: endonexin fold *status predicted
F:172-244/Domain: annexin repeat homology <AXI>
F:18-100-116/Region: endonexin fold *status predicted
F:172-244/Domain: annexin repeat homology <AXI>
F:28-139/Domain: annexin fold *status predicted
F:28-219/Region: endonexin fold *status predicted
F:275-275/Region: endonexin fold *status (by protein kinase C) *status predicted
F:125,245/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL 73
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                                                                                                                         KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGPQIEETIDRETSGNLEQLLLAVVKSIR
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A;Residues: 29-44;72-77;112-119;163-180;181-190;226-235 <SOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.8%; Score 914; DB 1;
58.0%; Pred. No. 1.8e-51;
iive 51; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:11111 | | ||
311 GEYKKALLKI,CGGDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 GDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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182; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annexin IV - bovine
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A. Reference number: $23447
A. Reference number: $23447
A. Reference number: $23447
A. Molecule type: mRNA
A. Residues: 1-505 < TON>
A. Residues: 1-505 < TON>
A. Residues: 1-505 < TON>
A. COSSION: SEMBL: $211742; NID: 977; PIDN: CAA77801.1; PID: 978
A. Cross references: EMBL: $213-226, 1992
A. Towle. C. A.; Welssbach, L.; Treadwell, B. V.
Biochim. Biophys. Acta 1131, 223-226, 1992
A. Towle. C. A.; Welssbach, L.; Treadwell, B. V.
Biochim. Sionys. Acta 1131, 223-226, 1992
A. Towle. C. A.; Welssbach, L.; Treadwell, B. V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 KOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72
                                                                                                                                         C;Date: 22-Nov-1993 #sequence_revision 10-Feb-1995 #text_change 22-Jun-1999 C;Accession: S23447; S36136 R;Towle, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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F;61,113/Binding site: carbohydrate (Asn) (covalent) *status predicted
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N;Alternate names: calcyclin-associated annexin protein CAP-50
C;Species: Oryctolagus cuniculus (domestic rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 52.8%; Score 865; DB 1; Length 50 Local Similarity 54.9%; Pred. No. 4.3e-48; hes 173; Conservative 58; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, note: the list of introns is incomplete
C, Superfamily: annexin repeat homology
C, Superfamily: annexin repeat homology
C, Reywords: alternative splicing: calcium binding; dup.
F; 203-274/Domain: annexin repeat homology <AX1>
F; 246/Domain: annexin repeat homology <AX2>
F; 246/Domain: annexin repeat homology <AX2>
F; 356-302/Region: endonexin fold #status predicted
F; 358-430/Domain: annexin repeat homology <AX3>
F; 358-430/Domain: annexin repeat homology <AX3>
F; 356-430/Domain: annexin repeat homology <AX3>
F; 347-505/Domain: endonexin fold #status predicted
F; 445-461/Region: endonexin fold #status predicted
                                                                                                                                      C; Species: Bos primigenius taurus (cattle)
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C;Genetics:
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Matches
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A; Residues: 213-223, X', 225-226;319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-339;441-450, 'X',
A; Experimental source: lung
A; Note: sequence modified after extraction from NCBI backbone
C; Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-503 <TOM>
A; Residues: 1-503 <TOM>
A; Cross-references: GB:MB2802; NID:g162673; PIDN:AAA30379.1; PID:g162674
A; Cross-references: GB:MB2802; NID:g162673; PIDN:AAA30379.1; PID:g162674
A; Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi, R.; Hidaka, A; Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi, R.; Hidaka, A; Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblast A; Reference number: A42909; MUID:92317074; PMID:1618851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fold; glycoprotein; phospholipid bin
                                                                                                                                                                                                N'Alternate names: calcyclin-associated protein peptide, CAP-50
C.Species: Bos primigenius taurus (cattle)
C.Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C.Accession: A42113; A42909; B42909; C42909; D42909
R.TOWLe, C.A.; Treadwell, B.V.
J. Biol. Chem. 267, S416-5423, 1992
A;Title: Identification of a novel mammalian annexin. cDNA cloning, sequence analysis, A;Reference number: A42113; MUID:92184796; PMID:1372001
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A.Note: the list of introns is incomplete
C.Superfamily: annexin vI; annexin repeat homology
C.Keywords: calcium binding; duplication; endonexin fold; glycoprotein;
F.201-272/Domain: annexin repeat homology <AXI>
F.212-228/Region: endonexin fold #status predicted
F.233-44/Domain: annexin repeat homology <AXI>
F.384-300/Region: endonexin fold #status predicted
F.385-384/Region: endonexin fold #status predicted
F.356-384/Romain: annexin repeat homology <AXI>
F.386-384/Region: endonexin fold #status predicted
F.432-503/Domain: annexin repeat homology <AXI>
F.443-459/Region: endonexin fold #status predicted
F.431-503/Domain: annexin repeat homology caxis
F.443-459/Region: endonexin fold #status predicted
F.59,111/Binding site: carbohydrate (Asn) (covalent) #status predicted
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. 4.3e-48;
. . 84; Indels
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   DTSGEYKKALLKLCEGDDD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 54.9%;
Matches 173; Conservative 5
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GDYRKILLKICGGND 503
                                                                                                                                                                     form A · bovine
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306
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Gaps

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Indels

72

192

370 252

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fold; glycoprotein; phospholipid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                      A; Cross-references: GB:L19605; NID:g457128; PIDN:AAA19734.1; PID:g457129
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
                                                                                                                                                                                                                           A.Map position: 9q11-9q22
C;Superfamily: annexin VII; annexin repeat homology
C;Reywords: calcium binding; duplication; endonexin
F;203-274/Domain: annexin repeat homology <AXI>F;275-346/Domain: annexin repeat homology <AXI>F;358-430/Domain: annexin repeat homology <AXI>F;358-430/Domain: annexin repeat homology <AXI>F;434-505/Domain: annexin repeat homology <AXI
                                                                                                                                                                                                                                                                                                                                                                                                                           52.2%; Score 855; DB 2; 53.3%; Pred. No. 1.9e-47, iive 61; Mismatches 8
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ne : 17 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                   A; Cross-references: GDB:313076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 168; Conserv
                                                                         A; Molecule type: mRNA
A; Residues: 1-505 <MIS>
                                                    A;Status: preliminary
                                                                                                                                                                              A; Gene: GDB: ANX11
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A.Residues: 104-141;213-223, 'X',225-231;254-263;271-280;285-291,'X',293-300,'X',302-309;
C.Comment: This protein binds specifically to calcyclin in a Ca2+ dependent manner.
C.Superfamily: annexin VII; annexin repeat homology fold; glycoprotein; phospholipid bin C.Superfamily: annexin repeat homology AXI>
C.Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin F.201-272.Domain: annexin repeat homology AXI>
F.201-272.Domain: annexin repeat homology AXI>
F.201-373-344.Domain: annexin repeat homology AXI>
F.364-300/Region: endonexin fold #status predicted
F.368-384.Meagion: endonexin fold #status predicted
F.368-384.Meagion: endonexin fold #status predicted
F.433-673.Domain: annexin repeat homology AXI>
F.368-Blanding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                  A.Accession: PH0950
A.Accession: PH0950
A.Molecule type: protein
A.Realdues: 104-141.213-213.254-262:270-280;285-309;319-337;429-448;478-492 <FK2>
A.Realdues: 104-141.213-213.231;254-262:270-280;285-309;319-337;429-448;478-492 <FK2>
R.Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.
A. Biol. Chem. 267, 8919-8924, 1992
A.Title: A calcyclin-associated protein is a newly identified member of the Ca(2+)/phosp
A.Reference number: A38250; MUID:92250478; PMID:1533622
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000 C; Accession: JH0694; PH0950; A38250; PS0263 B; Tokumitsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H. Biocham Biochys. Res. Commun. 186, 1227-1235, 1992 A; Title: Molecular cloning of rabbit CAP-50, a calcyclin-associated annexin protein. A; Reference number: JH0694; MuID:92378579; PMID:1380798
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C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 13-Aug-1999
C;Accession: A53152
R;Misaki, Y.; Prulijn, G.J.M.; van der Kemp, A.W.C.M.; van Venrooij, W.J.
J; Biol. Chem. 269, 4240-4246, 1994
A;Title: The 56K autoantigen is identical to human annexin XI.
A;Reference number: A53152; MUID:94140847; PMID:7508441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                           A:Cross-references: DDBJ:D10883; NID:g471147; PIDN:BAA01705.1; PID:g471148
A:Experimental source: lung
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Pred. No. 5.7e-48;
60; Mismatches 84
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                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-503 <TOK>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 22, 2003, 21:28:42 ; Search time 8.66667 Seconds (Without alignments) 1774.354 Million cell updates/sec Run on:

US-09-970-969-2 1639 1 MACGGGHMAQVLRGTVTDFP......KGDTSGDYKKALLLLSGEDD 327 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	8758 homo s	P81287 bos taurus	P48036 mus musculu	rattus	P17153 gallus gall	cynops	homo sa	mus m	. P09525 homo sapien	s sns	P48037 rattus norv	P97429 mus musculu	P13214 bos taurus	canis	P51901 gallus gall	rattus	P27214 bos taurus	P33477 oryctolagus		mus m	Snu	рошо	homo	O35639 mus musculu	рошо	Q07076 mus musculu		P79134 bos taurus	hydra a		P22464 drosophila	P07355 homo sapien	P04272 bos taurus	
SUMMARIES		qı	ANX5_HUMAN	ANX5_BOVIN	ANX5_MOUSE	ANX5_RAT	ANX5_CHICK	ANX5_CYNPY	ANX6_HUMAN	ANX6_MOUSE	ANX4_HUMAN	ANX4_PIG	ANX6_RAT	ANX4_MOUSE	ANX4_BOVIN	ANX4_CANFA	ANX6_CHICK	ANX4_RAT	ANXB_BOVIN	ANXB_RABIT	ANXB_HUMAN	ANXB_MOUSE	ANX8_MOUSE	ANX8_HUMAN	ANX3_HUMAN	ANX3_MOUSE	ANX7_HUMAN	ANX7_MOUSE	ANX3_RAT	ANX6_BOVIN	ANXC_HYDAT	ANX7_XENLA	ANX9_DROME	ANX2_HUMAN	ANX2_BOVIN	
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007936 rattus norv P07356 mus musculu P22465 drosophila P27216 homo sapien P27006 xenopus lae Q24471 canis famil P17785 gallus gall P24801 xenopus lae P51662 oryctolagus P14087 caria cutle P04083 homo sapien P46193 bos taurus	
ANX2_RAT ANX2_MOUSE ANX2_MOUSE ANXD_HUMAN ANXB_XENIA ANXB_XENIA ANX2_CANFA ANX2_XENIA ANX1_RABIT ANX1_RABIT ANX1_LAVU ANX1_LAVU ANX1_LAVU ANX1_BOUIN	
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ALIGNMENTS

ANXS_HUMAN TID ANXX_HUMAN STANDARD; PRT; 319 AA.	01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 09, Last sequence update) 15-550-7003 (Rel. 09, Last sequence update)		(Thrombo) lastin inhibitor) (Vascular anticoagulant-	ANXAS OR ANXS	Homo sapiens (Human). Eukaryota; Metazoa; Chordata;	OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		RP SEQUENCE FROM N.A. REPLINE-88234495: Pubmed-2967495:		RA Kuepper H.; RT "Characterization of cDNA encoding human placental anticoagulant	protein (PP4): homology with the lipocortin family.		RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.		RA Stratowa C., Hauptmann R.; Dr "Cloning and expression of onna for human wascular antiocasulant a	Ca2+-dependent phospholipid-binding protein.";	Eur. J. Blochem. 174:585-592(198	RP SEQUENCE FROM N. B.	MEDLINE-88273202; Pubmed-2968983;		Hession C., Frey A.Z., Wallner B.P.;	RT "Five distinct calcium and phospholipid binding proteins snare pm homology with lingertin T ".			RP SEQUENCE FROM N.A. RX MEDLINE-88163463: PubMed-2964863:	Funakoshi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;	RT "Primary structure of human placental anticoagulant protein.";		RP SEQUENCE FROM N.A., AND SEQUENCE.	RX MEDLINE-88139278; PubMed-2963810; Da Tungabi a Suda M Nabac W Nacowa W Sainc V Arai W	Mizoguchi T., Sato F., Yoshizaki H., Hi	RA Shidara Y., Murata M., Maki M.; RT "Structure and expression of cDNA for an inhibitor of blood		_
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MEDLINE-91065314; PubMed-2147412;

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TISSUE-Muscle, Ovary, and Skin;

WEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; PubMed-12477932;

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A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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Richards S.A., McEwan P.J., McKernan R.J., Lu X., Glubs R.A.,

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TISSUE-Lung;
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X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)

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MEDLINE-98062349; PubMed-9398511;
                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                               MEDLINE-91085549; PubMed-2148156;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 40, Lipocortin V) (Endonexin II) (Calphobindin I) (CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha)
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"Novel isoforms of CaBP 33/37 (annexin V) from mammalian brain:

"Novel isoforms of CaBP 33/37 (annexin V) from mammalian brain:

"The structural and phosphorylation differences that suggest distinct blood cal roles.";

Biochim. Blophys. Acta 1160:76-83(1992).

"HOLOGICAL THIS PROPEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.

"SUBUNIT: MONOMER. BINDS ATRX (By similarity).

"I- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

"I- SIMILARITY: GELONGS TO THE ANNEXIN FAMILY.

"I- SIMILARITY: Contains 4 annexin repeats.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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MEDLINE-93041974; PubMed-1420335;
Learmonth M.P., Howell S.A., Harris A.C.M., Amess B., Patel Y.,
Glambanco I., Bianchi R., Pula G., Ceccarelli P., Donato R.,
                                                                ö
                   Length 319;
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                   Score 1585; DB 1;
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Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProCom; PD000143; Annexin; 4.
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mes 318; Conservative
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Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                                                                                                                                                                                                                                                                                                                  AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
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Welkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus NCBI_TaxID=10090;
Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation; Acetylation.
REPEAT 23 83 ANNEXIN 1
REPEAT 95 155
REPEAT 170
REPEAT 170
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                                                                                                                                                                                                                                            DB 1; Length 320;
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
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TISSUE-Peritoneal cavity;
BIDLINE-96422179; PubMed-8824796;
Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez "Mouse annexin V chromosomal localization, cDNA sequence conservation, and molecular evolution.";
                                                                                                                                                                                                                                           Score 1536.5; DB 1; Length
Pred. No. 2.1e-92;
5; Mismatches 5; Indels
                                                                                                                                                                          ACETYLATION (BY SIMILARITY)
                                                                                                                                                                                                                 50FCE18E95F19CB0 CRC64;
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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SEQUENCE FROM N.A.
STRAIN-129/SvJ; TISSUE-Liver;
                                                                                                                                                                                                                    35942 MW;
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                                                                                                                                                                                                                                                                      Matches 309; Conservative
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                                                                                                                                                                                                                    320 AA;
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SEQUENCE FROM N.A.
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179
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us-09-970-969-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                        BIOCHEM. 337:125-131(1999).
FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
SUBBUNIT: MONOMER. BINDS ATRX (By similarity).
DOMAIN: A pair of annexin repeats may form one binding site for each clum and phospholipid.
SIMILARITY: BELCOMGS TO THE ANNEXIN FAMILY.
SIMILARITY: CONTAINS 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
            Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.R., Bances P.,
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                                    "Mouse annexin V genomic organization includes an endogenous
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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94 154 AN
178 238 AN
253 313 AN
319 AA; 35752 MW;
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InterPro: IPR001464; Annexin.
Pfam: PF00191; annexin; 4.
PRINTS: PR00195; ANNEXIN; 4.
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                                                  retrovirus."
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                  SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
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15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin AS (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PPA)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Swairjo M.A., Concha N.O., Kaetzel M.A., Dedman J.R., Seaton B.A.; "Caf'c*!- bridging mechanism and phospholipid head group recognition in the membrane-binding protein annaxin V."; Nat. Struct. Biol. 2:968-974(1995).
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STRAIN-Wistar: TISSUE-Brain;
MEDLINE-96301899; PubMed-8667030;
Ohsawa K., Imal Y., Ito D., Kohsaka S.;
"Molecular cloning and characterization of annexin V-binding proteins
                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"Structure of rat annexin V gene and molecular diversity of 1ts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93369587; PubMed-8362244; Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.; Rat annexin V crystal structure: Ca(2+)-induced conformational
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
MEDLINE=88273202; PubMed=2968983;
MEDLINE=88273202; PubMed=2968983;
Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S.,
Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
Flive distinct calcium and phospholipid binding proteins share homology with lipocortin I.*,
J. Blol. Chem. 263:10799-10811(1988).
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MEDLINE-96035863; PubMed-7556178;
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MEDLINE-96069783; PubMed-7583670;
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304 GDYKKALLLLCGGEDD
                                                                       GDYKKALLLL-SGEDD
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01-FEB-1996 (
15-SEP-2003 (
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P17153;
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license afreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  with highly hydrophilic peptide structure.";
J. Meurochem. 67:89-97(1996).
-1- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS
AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
-1- SUBUNIT: MONOMER. Binds ATRX and DNWT1.
-1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                                    calcium and phospholipid.
SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                           , M21730; AAA41512.1; -, D42137; BAA07708.1; -, D42129; BAA07708.1; -, D42130; BAA07708.1; -, D63137; BAA07708.1; -, D63137; BAA07708.1; -, JOINED.; D42131; BAA07708.1; -, JOINED.; -, D42132; BAA07708.1; -, JOINED.
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Pfam; PF00191; annexin; 4.
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BAA07708.1; J
BAA07708.1; J
BAA07708.1; J
BAA07708.1; J
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1A8A; 17-JUN-98.
1A8B; 17-JUN-98.
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PIR, C29250; LURTS
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01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                         Gaps
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SECULINE-88186917; PubMed=2833522;
MEDLINE-88186917; PubMed=2833522;
Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
Deutzmann R., Mollenhauer J., von der Mark K.;
"The structure of anchorin CII, a collagen binding protein isolated
"The orndrocyte membrane.";
J. Biol. Chem. 263:5921-5925(1988).
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                                                                                                                                                                                                                                 35613 MW; 1A755A7C11FA11CE CRC64;
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Matches 291; Conservative
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RX MEDLINE-93229489; PubMed-8471604;

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RL Structure of chicken annexin vat 2.25-A resolution.";

RL BIOCHEMISTY 32:3923-3929(1993).

CC '-- FUNTION: COLLAGEN BINDING PROTEIN.

CC Calcium and phospholipid.

CC '-- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

CC '-- SIMILARITY: Contains 4 annexin repeats.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration of the European bioinformatics institute. There are no restrictions on its content is statement is not removed. Usage by and for commercial contains a requirement is not removed. Usage by and for commercial containts requires a licensee 4180-41b.ch).
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from chondrocyte membrane.;
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MEDLINE-94115900; PubMed-8163186;
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Blochem. J. 291:601-608(1993).
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EMBO J. 9:1336-1336(1990).
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
D -> E (IN REF. 1).
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PDB; JALA, 31-OCT-93.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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E; PS00223; ANNEXIN; 4.
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                                                                                                                                   128 ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                188 QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                               8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynopa.
NCBI_Taxib-8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Tamamoto T., Hikono T., Abe S.I.;
"Differential expression of annexin V during spermatogenesis in the newt Cynops pyrrhogaster.";
Dev. Genes Evol. 206:64-71(1996).
                                                                          ö
                                      Length 321;
                                                                          Indels
36198 MW; 43E2983F86797025 CRC64;
                                      DB 1;
                                                      ; Pred. No. 8.6e-76; 38; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Innexin AS (Annexin V).
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                                      78.0%; Score 1279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGDTSGDYKKALLLLSGEDD 327 : 111111:111111 | 11 | QKDTSGDYRKALLLLCGGDD 320
                                                                          Conservative
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321 AA;
                                                      Best Local Similarity
Matches 250; Conserv
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SEQUENCE
   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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         MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY). DOMAIN: A pair of annexin repeats may form one binding site for
FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-A0G-1988 (Rel. 08, Created)
1-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocottin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens (Human).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                            66.5%; Score 1090.5; DB 1; Length 323; 66.7%; Pred. No. 1.3e-63; ive 45; Mismatches 59; Indels 5;
                                                                                                                                                                                                                                                                                            ANNEXIN 4.
044B31AC28164CE2 CRC64;
                             calcium and phospholipid.
SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
SIMILARITY: Contains 4 annexin repeats.
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ANNEXIN 3.
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                                                                                                                                                                                             Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                  InterPro; IPR001464; Annexin.
                                                                                                                                                             EMBL; D64134; BAA11012.1; -. HSSP; P08758; 1AVH.
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PROSITE; PS00223; ANNEXIN; 4.
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P08133;
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MEDINE-22388257; PubMed-12477932;

X. TISSUE-Tetrus;

X. MEDINE-22388257; PubMed-12477932;

X. Ridusher R.D., Felngold E.A., Grouse L.H., Derge J.G.,

X. Ridusher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A nothing R.L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Scheetz T.E.,

X. Donnstein M.J., Osdin T.B., Toshlywik S., Carnina P. Prange C.,

X. Bronstein M.J., Osdin T.B., Toshlywik S., Carnina P. M.,

Ruba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Richards S., Worley K.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Raha S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Hilalon D.K., Muzny D.M., Scharden A., Rodrigues S., Sanchez A.,

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R. Hilalon A., Youchman J.W., Schautz J., Myers R.M.,

R. Blakesley R.W., Touchman J.W., Schautz J., Myers R.M.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Donnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Generation and initial analysis of more than 15,000 full-length

R. Donnerch A. Schein D. S. Dones S.J.M., Marra M.A.,

R. Donner A., Schein D.M. Septences.";

R. Donner A., Schein D. S., Schein D. S., Schein D. S.,

R. Donner A., Schein D. S., Schein D. S., Schein D. S.,

R. Donner A., Schein D. S., Schein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suedhof T.C., Slaughter C.A., Leznicki I., Barjon P., Reynolds G.A.; "Human 67-kDa calelectrin contains a duplication of four repeats
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-i- MISCELLANEDOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
-i- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-i- SIMILARITY: CONTAINS 8 ONDEXIN FE
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-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
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                                                                                                                                                                                                                                                    "Primary structure of the human, membrane-associated Ca2+-binding protein p68 a novel member of a protein family."; EMBO J. 7:21-27(1988).
[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDINE-88196081; PubMed=3258820; Crompton M.R., Owens R.J., Totty N.F., Moss S.E., Waterfield M.D. Crumpton M.J.; Fram human, membrane-associated Ca2+-binding
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Benz J., Bergner A., Hofmann A., Demange P., Goettig P., Liemann
Huber R., Voges D.;
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MEDLINE-89380132; PubMed-2528541;
MEDLINE-89380132; PubMed-2528541;
Iwasaki A., Suda M., Watanabe M., Nakao H., Hattori Y., Nagoya Saino Y., Shidara Y., Maki M.;
Siructure and expression of cDNA for calphobindin II, a human placental coagulation inhibitor.";
J. Biochem. 106:43-49(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found in 35-kDa lipocortins.";
Proc. Natl. Acad. Sci. U.S.A. 85:664-668(1988).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ANNEXIN 2.

ANNEXIN 3.

ANNEXIN 4.

ANNEXIN 5.

ANNEXIN 6.

ANNEXIN 7.

ANNEXIN 8.

ACETYLATION.

IE -> MK (IN REF. 2).

IE -> MK (IN REF. 2).

E -> D (IN REF. 1).

E -> D (IN REF. 1).

W; 2829237029BDIDCB CRC64;
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                                                                                                                                      EMBL; D00510; BAA00400.1; -...
EMBL; Y00097; AAA35656.1; -...
EMBL; BC017046; AAA17046.1; -...
PIR; JU0032; AQHU68.
PDB; IM91: 07-AUG-02.
Genew; HGNC:544; ANXA6.
MIM; 114070; -...
InterPro; IPR001464; Annexin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75742 MW;
                                                                                                                                                                                                                                                                                                   Pfam; PF00191; annexin; 8.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
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554
618
672 AA;
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SEQUENCE
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ID ANX6_M(
AC P14824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-i- MISCELLANGOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
-i- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                          Moss S.E., Crompton M.R., Crumpton M.J.;
"Molecular cloning of murine p68, a Ca2+-binding protein of the
lipocortin family.";
Eur. J. Biochem. 177:21-27(1988).
--i- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF
CA(2+) FROM INTRACELLULAR STORES.
                     15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)
                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 6.
ANNEXIN 7.
ANNEXIN 7.
ANNEXIN 8.
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59.0%; Pred. No. 5.2e-53;
ive 49; Mismatches 80
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01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
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ProDom; PD000143; Annexin; 8.
SMART; SM00135; ANX; 8.
PROSITE; PS00223; ANNEXIN; 8.
Annexin; Calcium/phospholipid-binding; 1
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MEDLINE-89030687; PubMed-2972541;
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MGD; MGI:88255, Anxa6.
InterPro; IPR01464; Annexin.
Pfan; PF00191; annexin; 8.
PRINTS; PR00196; ANNEXIN.
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Best Local Similarity 59.00
Matches 186; Conservative
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532
607
672 AA;
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                                                                                                                                                                                                         NCBI_TaxID=10090;
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100
184
259
                                                                                                    ANXA6 OR ANX6.
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RECEINGE-Eye, and Uterus;

RECEINGE-Eye, and Uterus;

REDIINE-2238825; PubMed-12477932;

REDIINE-2238825; PubMed-12477932;

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uddin T.B., Toshlywik S., Carninol P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Roha S.S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willialon D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Williting M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schelu J.E., Jones S.J.M., Marra M.A.;

Ra Generation and Initial analysis of more than 15,000 full-length
190 KWGTDEAQFIYILGNRSKQHLRLVFDEYLKTTGKPIEASIRGELSGDFEKLMLAVVKCIR 249
                                                                                                                                                                                                                                                                                                              ANX4_HUMAN STANDARD; PRT; 318 AA.
P09525; Q9663; Q96813; Q9BWKL;
01-MAR-1989 (Rel. 10, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
(Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II)
(PP4.X) (35-beta calcimedin) (Carbohydrate-binding protein P33/P41)
                                                SIPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-8830902; PubMed-2970257;
Grundmann U., Amann E., Abel K.-J., Kuepper H.A.;
"Isolation and expression of colon colon phospholipase A2 inhibitor family.";
Phospholipase A2 inhibitor family.";
Behring Inst. Mitt. 82:59-67(1988).
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Biol. Pharm. Bull. 20:224-229(1997).
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MEDLINE-97239215; PubMed-9084877;
Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92155721; PubMed-1346776;
Talt J.F., Smith C., Frankenberry D.A., Miao C.H., Adler D.A.,
Disteche C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Chromosomal mapping of the human annexin IV (ANX4) gene."; Genomics 12:313-318(1992).
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310 GEYKKALLKLCGGDD 324
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                        "Sedimentation equilibrium analysis of five lipocortin-related phospholippes A2 inhibitors from human placenta. Evidence against a mechanistically relevant association between enzyme and inhibitor."; J. Biol. Chem. 263:18657-18663(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
-:- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-:- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human placental annexin IV.";
J. MOL. Biol. 216:219-221(1990).
-!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
MEMBERANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                                                                        MEDLINE-89066652; PubMed-2974032;
Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
de Haen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-91073383; PubMed-2254922; Freemont P.S., Driessen H.P.C., Verbi W., Crumpton M.J.; "Crystallization and preliminary X-ray crystallographic studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 8e-53;
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Hendrickson L.E., Fujikawa K.;
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16B19E01500350F7 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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Annexin; Calcium/phospholipid-binding;
                              [5]
SEQUENCE OF 26-55; 98-123 AND 279-307.
MEDITINE-89066652; PubMed-2974032;
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EMBL; M82809; AA51740.1; -.
EMBL; D78152; BAA11227.1; ALT_INIT.
EMBL; BC00182; AAH00182.1; ALT_INIT.
EMBL; BC011659; AAH11659.1; ALT_INIT.
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InterPro: IPR001464; Annexin.
Predan; Pr00191; annexin, 4.
PRINTS; Pr00195; ANNEXIN.
ProDom; PD000143; Annexin, 4.
SMART; SM00335; ANX; 4.
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35751 MW;
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SWISS-2DPAGE; P09525; HUMAN.
PMMA-2DPAGE; P09525; -.
Genew; HGNC:542; ANXA4.
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the European Bloinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
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I) (PAP-II)
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                                                                                                                    OVYEERYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
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Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for protein kinase C; the domain structure Ca2+-modulated lipid binding proteins.*; EMBO J. 6:1599-1604(1987).
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-calcium and phospholipid.
-i- MISCELLANGOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
-i- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-i- SIMILARITY: Contains 4 annexin repeats.
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TISSUE-Small intestine;

MEDLINE-9627607; PubMed-8672129;

Winterce A.K., Fredholm M., Davies W.;

"Evaluation and characterization of a porcine small intestine cDNA library; analysis of 839 clones.";

Mamm. Genome 7:809-517(1996).

-!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).

-:- SUBUNIT: Monomer.
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Mammalla; Eutherla; Cetartlodactyla; Suina; Suidae; Sus.
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PNS4_PIG Sim.
P08132; 029306;
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-30141, Last annotation update)
28-FEB-3015 (Rel. 17) (Lipocortin IV) (Endonexin IV) (Lipocortin IV) (Endonexin IV) (Lipocortin IV) (L
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MEDLINE-87275850; PubMed-2956093;
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostom1;
Mammalia: Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE-55313131; PubMed-7607247;
Fan H., Josic D., Lim Y.P., Reutter W.;
Fan Cloning and tissue-specific regulation of expression of rat calcium-binding protein 65/67. Identification as a homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III) (Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)
                                                                                                       PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
Acetylation.
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                                                                                                                                                                                                                                                                                               Length 318;
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PHOSPHORYLATION (BY PKC).
FA7D9CE2B7C631E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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ANNEXIN 2.
ANNEXIN 3.
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                         InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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305 DYRKVLLILCGGDD 318
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Best Local Similarity 58.69
Matches 184; Conservative
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PIR; A27107; LUPG4
HSSP; P13214; 1ANN
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P48037;
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STRAIN-C3H/HeJ;
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                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
                          MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY. SIMILARITY: BELONGS TO THE ANNEXIN FAMILY. SIMILARITY: Contains 8 annexin repeats.
         DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
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                                                                                                                                                                                                                                                                                                                                                       Length 672;
                                                                                                                                                                                                                                                                                                                                                                           82; Indels
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 6.
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ANNEXIN 6.
ANNEXIN 8.
ANNEXIN 8.
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                                                                                                                                                                   InterPro; IPR001464; Annexin.
Pam; PF00191; annexin.
PRINTS; PR00196; ANNEXIN.
PRODOM; PD000143; Annexin; 8.
SWART; SM00335; ANX; 8.
ANNEXIN; PS00223; ANNEXIN; 7.
ANNEXIN; Calcium/phospholipid-binding; Repeat.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                    75622 MW;
                                                                                                                                          EMBL; X86086; CAA60040.1; -. PIR; S65683; S52844.
HSSP; P79134; 1AVC.
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GEYKKALLKLCGGDD 324
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160
244
319
431
503
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01-NOV-1997 (
28-FEB-2003 (
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ANX4_MOUSE
ID ANX4_MOUSE
AC P97429;
DT 01-NOV-1997
DT 01-NOV-1997
DT 28-FEB-2003
DE Annexin A4 (
                                                                                                                                                                                                                                                                                                                                                                        Matches 185;
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                                                                                                                                                                          Sable C.L., Shannon J., Riches D.W.H.;
Submitted (JAN-197) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-197) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CALCIUM/PHOSHOLIPID-BINDING PROTEIN WHICH PROMOTES
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; ευτειευευσισιτί;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                   Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.9%; Score 916; DB 1; 57.3%; Pred. No. 2.3e-52;
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BY SIMILARITY.
ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-1- SIMILARITY: Contains 4 annexin repeats.
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SMART; SM00335; ANX; ANX
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid_binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 82 AN
94 154 AN
178 238 AN
253 313 AN
318 AA; 35858 WW;
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InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
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ProDom; PD000143; Annexin; 4.
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Mus musculus (Mouse)
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SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=10090;
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Annexin;
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                                                01-JAN-1990 (Rel. 13, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
(Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II)
(PP33/41).
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-96205957; Pubmed-8631806;
MEDLINE-96205957; Pubmed-8631806;
MEDLINE-96205957; Pubmed-8631806;
Midliam K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;
"Characterization of carbohydrate-binding protein p33/41: relation
with annexin IV, molecular basis of the doublet forms (p33 and p41),
and modulation of the carbohydrate binding activity by
phospholipids.";
J. Biol. Chem. 271:7679-7685(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                         TISSUE-Liver;
MEDLINE-89050088; PubMed-2847715;
Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.;
"Cloning and characterization of a cDNA encoding bovine endonexin
                                                                                                                                                                                                                                                      (chromobindin 4).";
Biochem. Biophys. Res. Commun. 156:660-667(1988).
                    318 AA.
                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
Sutton R.B., Sprang S.R.;
Submitted (SEP-1995) to the PDB data bank.
                                       01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22248; AAA30507.1; -.
EMBL; X13627; CAA31954.1; -.
EMBL; D78178; BAA11243.1; -.
PIR; A31578; LUBO4.
PDB; 1ANN; 29.JAN-96.
PDB; 1AOW; 14-JAN-98.
PDB; 114A; 25.APR-01.
InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfan, PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
PLODOM; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                      ANXA4 OR ANX4.
                   ANX4_BOVIN
P13214;
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194 WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last sequence update)
Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule membrane associated protein) (2AP36).
ANXA4 OR ANX4.
Canis familiaris (Dog).
Calcium/phospholipid-binding; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 318;
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                                                                            25.
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Best Local Similarity 58.0%; Pred. No. 3e-52;
Matches 182; Conservative 51; Mismatches
                                                                            REF.
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                        ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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E -> K (IN R
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                                                                                                                ANX4_CANFA
P50994;
          INIT_MET
REPEAT
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRARME FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).

-1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

-1- MISCELLANBOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
Chordata; Craniata; Vertebrata; Euteleostomi;
Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 901; DB 1; Length 31; Pred. No. 2.1e-51; 54; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            42EF5B89179B4863 CRC64;
                                                                                                                                             SIMILARITY: BELONGS TO THE ANNEXIN FAMILY. SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                              Annexin; Calcium/phospholipid-binding; Repeat.
INIT_MET 0 0 BY SIMILARITY.
REPEAT 22 82 ANNEXIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671 AA.
                                                                                                                                                                                                                                                                                                                                                                             ANNEXIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                  ANNEXIN 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                   STRAIN-Mongrel; TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
Procom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                             35681 MW;
                                                                                                                                                                                                                                                            EMBL; D38223; BAA07398.1; -. HSSP; P13214; 1ANN.
                                                                                                                                                                                                                                                                                                                                   PS00223; ANNEXIN; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%;
57.0%;
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DYRKVLLICGGDD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     178 2
253 3
318 AA;
 Eukaryota; Metazoa;
          Eutheria;
                                                                                                                                   (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANX6_CHICK
ID ANX6_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314
                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305
                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
                                                              Fukuoka
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                            REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KVYRGSVKDFPGFNASQDADALCNAMKGFGSDKDAILDLITSRSNKQRLEICQAYKSQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 GELKWGIDEEKFITIFGIRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVK
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94092130. PubMed-8267590;

Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman R.M., Wuthler R.E.;

"Characterization, cloning and expression of the 67-kDA annexin from chicken growth plate cartilage matrix vesicles.";

Blochem. Biophys. Res. Commun. 197:556-561(1993).

-I- FUNCTION: MAY RASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF CA(2+) FROM INTRACELLULAR STORES (BY SIMILARITY).

-I- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
19-SEP-2003 (Rel. 42, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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InterPro: IRR001464; Annexin.
Pram: PF00191; annexin; 8.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000113; Annexin; 8.
SMART; SM0035; ANN.
ANNEXIN; S800223; ANNEXIN; 5.
ANNEXIN; Calcium/Phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1e-50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 896.5;
Pred. No. 1e-
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ANNEXIN 4.
ANNEXIN 5.
ANNEXIN 6.
ANNEXIN 6.
ANNEXIN 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S67466; AAB29337.2; -. PIR; JC2029; JC2029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3est Local Similarity 57.74
Matches 184; Conservative
                                                                                                                                                                                                                                                                                                           Sallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9031;
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Search completed: August 22, 2003, 21:33:37 Job time : 10.6667 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

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August 22, 2003, 21:29:22 ; Search time 31.6667 Seconds
(without alignments)
2664.733 Million cell updates/sec
2664.733 Million cell updates/sec
1639
Sequence:
1 US-09-970-969-2
Sequence:
1 UACGGGHMAQVLRGTVTDFP......KGDTSGDYKKALLLLSGEDD 327
Scoring table:
1 BLOSUMG2
Gapop 10.0 , Gapext 0.5
Searched:
1 B10525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters:
1 Rinimum DB seq length: 2000000000
Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries
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4: sp_luman:* 5: sp_luman:* 6: sp_luman:* 7: sp_mnmal:* 9: sp_mnmal:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:* 14: sp_lanciassified:* 15: sp_rarcheap:* 16: sp_lanciassified:* 17: sp_lanciassified:* 18: sp_lanciassified:* 19: sp_lanciassified:* 10: sp_lanciassified:* 11: sp_lanciassified:* 12: sp_lanciassified:* 13: sp_lanciassified:* 14: sp_lanciassified:* 15: sp_lanciassified:* 16: sp_lanciassified:* 17: sp_lanciassified:* 17: sp_lanciassified:* 17: sp_lanciassified:* 18: sp_lanciassified:* 19: sp_lanciassified:* 10: sp_lanciassified:* 10: sp_lanciassified:* 11: sp_lanciassified:* 12: sp_lanciassified:* 13: sp_lanciassified:* 14: sp_lanciassified:* 15: sp_lanciassified:* 16: sp_lanciassified:* 17: sp_lanciassified:* 18: sp_lanciassified:* 18: sp_lanciassified:* 19: sp_lanciassified:* 10: sp_lanc

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œ	998			13	093444	093444 oryzias lat	
6	856			13	093447	093447 oryzias lat	
10	849			13	Q90X16	090x16 xenopus lae	
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463 11 Q8VIN2 463 11 Q8BP75 324 5 Q9NL61 324 5 Q8IG38 301 11 Q921D0	20000	323 5 09GNG6 324 5 09NL60 324 6 09SD3 339 4 08TBV2 339 11 09C217	11 6 13 13	314 13 092128 322 5 027864 415 11 088CV9 209 11 0885£2 317 5 027473 365 5 09XY89
770 47.0 769 46.9 752 45.9 752 45.9 3.5 45.4	729 44.5 720 44.5 715 43.6 714 43.6	4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6	44444400	25.5 38.2 582 35.5 73.5 35.5 57.2 34.9 540 32.9 528 32.2
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ALIGNMENTS

1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:*

SPTREMBL 23:*

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								Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	HOMO.						ses.	-! - DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING											Calcium; Calcium-binding; Calcium/phospholipid-binding;			Length 320;		Indels	SRSNAC
			,	ָ פ	ate)			ata;	idae;						lataba	ONE B											i pholi		CRC6				LTLL
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	. тад		Created)	rast sednence obdate)	Last annotation update)			rania	Catarrhin1; Hominidae;						Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.	EPEAT	CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).	SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.	XIN R	EMBL; BC018671; AAH18671.1;							ng; C		45FAC411DDBA4D1A CRC64;	Score 1585; DB 4;	ed.	0; Mismatches	TLRKA
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	ō	. 6	01-MAR-2002	OT-MAK-2002	01-MAR-2003	Annexin A5.	Homo sapiens (Human)	yota;	Mammalia; Eutheria;	NCBI_TaxID=9606;		SEQUENCE FROM N.A.	TISSUE-Skin;	Strausberg R.;	tted.	OMAIN	ALCIU	IMILA	SIMILA	BC01	InterPro; IPR001464; Annexin.	Pfam; PF00191; annexin; 4.	PRINTS; PR00196; ANNEXIN.	m; PD	SMO		rin; c	ıt.	SNCE	tch	al Si		ω-
- 58	ORWV69	Q8WV69;	01-MA	TO	01-M4	Annex	Homo	Eukar	Mamma	NCBI	[]	SEQUE	TISSL	Strac	Submi	-i -	J			EMBL;	Inter	Pfam;	PRINT	Prode	SMAR	PROS1	Annexin;	Repeat.	SEQUENCE	Query Match	Best Local Similarity	Matches	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 IKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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PROSITE; PS00223; ANNEXIN; 3.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Wen Y. Edelman J.L., Kang T., Sachs G.;
Wen Y. Edelman J. Edelman
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33965 MW; AB9FB40934A3D007 CRC64;
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Last annotation update)
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12;
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12; Mismatches
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92.0%; Pred. No. 1e-
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Pfam; PR00191; annexin; 4.
PRINTS; PR00196; ANNEXIN; 4.
Probom; PD000143; Annexin; 4.
                                                                                                                                      313 GDYKKALLLL-SGEDD 327
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23,
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01-AUG-1998 (TrEMBLrel. 07
01-AUG-1998 (TrEMBLrel. 07
01-MAR-2003 (TrEMBLrel. 22
Lipocortin V (Fragment).
Rattus norvegicus (Rat).
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Matches 276; Conserv
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SEQUENCE
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              124 KQVYEEEYGSNLEDDVVGDTSGYYQRMLVVLLQGNRDPDFAIDDAQVELDAQALFQAGEL
                                                                                                                                                                         188 QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319
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InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
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73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
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                                                                                                                                                                                          STRAIN-C57BL/63;
MEDLINE-22354683; PubMed=12466851;
The FANTOM CONSOrtium.
The RANGOM CONSOrtium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
The Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length choice.

The Manalysis of the Manalysis and The Manalysis of Annotation of 60,770 full-length choice.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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  23, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                             56.9%; Score 932; DB 11; 59.0%; Pred. No. 2.7e-57;
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MGD; MG1:88255; Anxa6.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 8.
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17,
23,
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01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                   Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Matthroad, J., Gerke V.;
Characterization and developmentally regulated expression of four anneans in the Xillifish medaka.";
DNA Cell Biol. 17:835-847(1998).
-I- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIDM AND PHOSPHOLIPID (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE ANNEXIN REPEATS.
-I- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
                                                                                                                                                                                                            Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Edxinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acauthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 AA; 34765 MW; AFD618681BAFF0FE CRC64;
                                                              093445 PRELIMINARY; PRT; 317 AA. 093445; 01-007-1998 (Tremelrel. 08, Last sequence update) 01-NOV-1998 (Tremelrel. 08, Last sequence update) 01-NOV-2003 (Tremelrel. 23, Last annotation update)
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64.4%; Pred. No. 2.9e-65;
ive 48; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
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QBCEXO;
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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HSSP; P17153; 1ALA.
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   133 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                    KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                   13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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Oryzlas latipes (Medaka fish) (Japanese ricefish).

Bukaryota: Metazoa; Chordata; Cranilata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei.
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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                                                                                                                                                                                                                                                              (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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; Pred. No. 6.5e-53;
59; Mismatches 83;
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PRINTS; PR00196; ANNEXIN.
ProDom; PB000143; Annexin; 4.
SWART; SW00335; ANX; 4.
ANNEXITE; PS00223; ANX; 4.
Annexin; Calcium; Calcium-binding;
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54.5%;
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Best Local Similarity 54.5'
Matches 170; Conservative
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                                                                                                                            Gaps
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MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium, The FANTOM Consortium, The FANTOM Consortium, The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation No.770 fulli-length cDNAs.";
Nature 420:563-873(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID-10090;
                                  PROSITE; PS00223; ANNEXIN; 8.
Annexin; Calcium; Calcium-binding; Calcium/Phospholipid-binding;
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                                                                          667 AA; 75260 MW; 363088A2A55CFF34 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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59.0%; Pred. No. 6.1e-57;
1ve 48; Mismatches 81;
                                                                                                 Score 932; DB 11;
Pred. No. 4.4e-57;
                                                                                                                          49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
                                                                                                  56.9%;
59.0%;
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311 GEYKKALLKLCGGDD 325
                                                                                                                            tches 186; Conservative
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                         SMART; SM00335; ANX; 8.
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hes 186; Conserv
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SEQUENCE FROM N.A.
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                                                                          SEQUENCE
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08BSS4;
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313 GDYKKALLLLSGEDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWGIDEEKFITIFGIRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
                 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                          72
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Osterloh D., Wittbrodt J., Gerke V.;
Characterization and developmentally regulated expression of four annexins in the killifish medaka.";
DNA Cell Biol. 17:835-847(1998).
-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                      Annexin max4.
Oryzias latipes (Medaka fish) (Japanese ricefish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000143; Annexin; 4. SMART; SM00335; ANX; 4. PROSITE; PS00223; ANNEXIN; 4. Annexin; Calcium; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 AA; 53051 MW; 3C6728D475CAE430 CRC64;
                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001464; Annexin.
InterPro; IPR006031; XYPPX.
Pfam; PF00191; annexin; 4.
Pfam; PF02162; XYPPX; 15.
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ProDom; PD000143; Annexin; 4.
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                                                                                                                          307 GDYRKILLELCG 318
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                 313 GDYKKALLLLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-8090;
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73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

A Seville R.A., wijjar S., Barnett M.W., Jones E.A.;

Tubules in Xenopus laevis.";

Lubules in Xenopus laevis.";

Calculum and PHOSPHOLIPID (BY SIMILARITY).

CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

CALCIUM AND PHOSPHOLIPID.

REMBL, ANO39235; AAK83461.1;

REMBL, AY039235; AAK83461.1;

RemBL, AY039235; PRO0136; ANNEXIN.

REMBL, PRO0196; ANNEXIN.

REMBL, PRO0196; ANNEXIN.

REMBL, PRODO196; ANNEXIN.

REMBL, ANDSO196; ANNEXIN.

REMBL, ANDSO196; ANNEXIN.
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                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.8%; Score 849; DB 13; Length 3 54.0%; Pred. No. 1e-51; ive 55; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5C28CAFAAC17687D CRC64;
                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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                                                                                                                                                              Ā
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                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                          Created)
                                                                                                                                                              PRT;
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                                            508
327
                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 54.0
Matches 170; Conservative
                             494 GDYKNLLLKLCGSSD
                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-8355
                                                                                                                                                                                                                                                                               Annexin 4
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NCBI_TaxID=9913
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RIGTDESKFNAILCSRSRAHLVAVFNEYQRMTGRDIEKSICREMSGDLEQGMLAVVKCLK 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                   Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-1-DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOILPID (BY SIMILARITY).

-1-SIMILARITY: BELLOGS TO THE ANNEXIN FAMILY.

-1-SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

EMBL, BC012875; AAH12875.1;

MGD: MGT:108481; AAR12.

InterPro: IPR001464; Annexin.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87; Indels
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Last sequence update)
Last annotation update)
  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.7%; Score 847; DB 11;
53.7%; Pred. No. 2.7e-51;
tive 59; Mismatches 87;
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                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
19,
23,
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GDYRKILLKICGGND 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169; Conservative
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01-DEC-2001 (TrEMBLrel.
                       (TrEMBLrel.
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                          Similar to annexin All.
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                                                                              Mus musculus (Mouse)
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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Matches 10
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Q8K2N9
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                                                                                                                                                                                                                                                                                                                                               82 GKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEYG 141
                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                               142 SSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELKWGTDEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201 FITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAE
                                                                                                                                                                                                                                                                          22 FDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSELT
                                                                                                                                                                                                                                        Gaps
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Bos taurus (Bovine).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthezia; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovinae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                        ï
                                                                                                                                                                                                   DB 11; Length 327;
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                                                                                                                                                                                                                                          Indels
EMBL/GenBank/DDBJ databases
                                                                                                                                                                 36724 MW; 56DB9CFAFA8C2B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36787 MW; 2EB178E13738CF22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                 51.3%; Score 840.5; DB 11;
57.8%; Pred. No. 4.2e-51;
1ve 49; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.0%; Score 836.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                 InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                      PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                                                                          PROSITE; PS00223; ANNEXIN; 4
SEQUENCE 327 AA; 36724 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00223; ANNEXIN; 4.
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             EMBL; BC030407; AAH30407.1;
MGD; MGI:1201374; Anxa8.
                                                                                                                                                                                                                                          Conservative
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                                                                                                                            SMART; SM00335; ANX; 4.
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PROSITE; PS00223; AN
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Best Local Similarity
Matches 177; Conserv
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 14 TVKGSPHFNPVPDAETLYKAMKGIGTNEQAIIDVLTRRSSAQRQQIAKSFKAQFGSDLTE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL: AR090055; BAC41070.1;
EMBL: AR090055; BAC41070.1;
SEQUENCE 323 AA; 36356 MW; 9F69F57BCFAC6A85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK
                                                                                                                                                             133 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIPAYLAETLYYAMKGAGTODHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                              WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.7%; Score 799; DB 11; Length 323;
49.2%; Pred. No. 3.3e-48;
Live 63; Mismatches 97; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                  323 AA.
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MEDLINE-22354683; PubMed-12466851;
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Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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Submitted (JUL.1997) to the EMBL/GenBank/DDBJ databases.
Li Submitted (JUL.1997) to the EMBL/GenBank/DDBJ databases.
Color of the EMBL/GenBank/DDBJ databases.
LI FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS AN INDIRECT INHIBITON OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH IN THE BLOOD COAGULATION CASCADE (BY SIMILARITY).
COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MITH A CONSENSUS SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. OF THE ANNEXIN FAMILY.
COMED SITE FOR CALCIUM AND PHOSPHOLIPID.
COMMON TO ALL ANNEXIN.
CHILARITY: TO OTHER PROTEINS OF THE ANNEXIN FAMILY.
CHARL, AFO12745; AAD01508.1; ----
INTEFPRO; IPRO01464; Annexin.
CHARL, PRO0191; Annexin.
CHARL, PRO0191; ANNEXIN.
CHARL, SMOO192; ANNEXIN.
CHARL, SMOO133; ANNEXIN.
CHARL, SMOO133; ANNEXIN.
CHARL, SMOO135; ANNEXIN.
CHARL, SMOO135; ANNEXIN.
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                                                                                                                                                                         254 IHGIFFAMKGAGTLDGTLIRNIVSRSEIDLNLIKNOFKKMYGKTLSSMIMEDISG 313
                                                                                                  DLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ 134
                                                                                                                                                          VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 193
                                                         15 TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD·74
                                                                                                                 TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD
                                                                                                                                                                                                                WCTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
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                  Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation.
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 Pred. No. 7.9e-51; . . 53; Mismatches 84; Indels
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Annexin A8 (Annexin 8) (Annexin VIII).
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 55.9%;
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Matches 175; Conservative
               175; Conservative
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Best Local Similarity
Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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Search completed: August 22, 2003, 21:35:24 Job time : 37.6667 secs

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1602)
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Emall: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Homo sapiens, clone IMAGE:3924873, mRNA.
BC032093
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                                                                              AL542496
BX358605
BX402751
AL517516
AL517516
AL516479
BU168479
BU368479
BX365074
BX265074
BX400530
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BX406330
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BX53799B21
BX537433
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BU167199
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BG767111
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Center code: BCM-HGSC
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Homo sapiens
USA
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8806.8
8906.8
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Š. Result

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ALS68578 ALS68578
BU168479 AGENCOURT
BX365074 BX365074
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Searched:

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Minimum | Maximum |

Database

Perfect score:

Sequence:

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Run

Scoring table:

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contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nlh.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhl.gov
Plate: LLAM1235 row: n column: 14
High quality sequence stop; 708.
Location/Qualifiers
i. 1076
/ organism="Homo sapiens"
// Ab_host="Homo sapiens"
// Lissue_type="miRNA"
// Ab_host="DH10B (phage-resistant)"
// Iab_host="DH10B (phage-resistant)"
// Iab_host="DH10B (phage-resistant)"
// Alone="InhMAGE: SA11; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
The contact of the color of the constructed by Life
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                          809 TTTCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTT
                                                                                        ATGAAGGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAG
                                                                                                                                                   ATTGATCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTTTATTCC
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                                                                                       Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 26 Row: f Column: 11
This clone has the following problem: no 5' EST match.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mnn.Na"
/db_xref="taxon:9606"
/clone="IMAGE:3924873"
/clone="Ib="NIH_MGC_72"
/lab_host="DH109"
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                               Score 958; DB 11;
Pred. No. 6.5e-246;
0; Mismatches 5;
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364 g 452 t
                            Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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Qy 82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 141 Db 165 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGAGCATCCTGACT 224 Qy 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201 Db 225 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 284 Qy 202 TTTGGCAGGAACTTCTGGATGACTGAAATCAGAACTAACT	09 322 AAGGGAGCTGGAACAATGAAAAGTACTGACGGAATTATTGCTTCAAGGACACCTGAA 381 1111111111111111111111111111111	Qy 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA 621 Db 645 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAAAGTTTATCACCATCTTTGGAACA 704 Qy 622 CGAAGTGTGTCCATTTGACAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 681 Db 705 CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAAGATTTCAA 764 Qy 682 ATTGAGGAAACCATTGACGAAAGGTGTTTGACAATTAGACAACTATATATA	Oy 742 GTGAAATCTATTCGAAGTATACCTGCCTACGAGACCCTGTATTATGCTATGAG 801	Qy 977 AT 978 1 1 1 1 Db 1065 AT 1066 RESULT 3 BX441583 1071 bp mRNA linear EST 15-MAY-2003 LOCUS BX441583 Homo sapiens FETAL BRAIN Homo sapiens cone CSDNA clone CSDNF019YK11 5-PRIME, mRNA sequence. ACCESSION BX441583 ACCESSION BX441583 LGI:30775951 GI:30775951

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BX417429 11301 bp mRNA linear EST 13-MAY-2003 BX417429 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE009Y116
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/note="lib" Homo sapiens primed with a NotI and enriched, double-strand cDNA was digasted with Not I and cloned into the Not I and EcoR v sites of the pCMVSPORT 6 vector. Library was normalized."
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BP 191 91006 EVRY cedex - France
Bmall: sequencecope.cns.fr.
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cg1?seq-CSOD1030DF09GP1&cluster-2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI030DF09GP1.
                                                                              TITCAAATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTT
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          GCTAACAGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCT
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                                                                TTATTTCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTT
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Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
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11, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                   15; Mismatches
 Score 858.4;
87.5%;
                  892; Conservative
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BX398791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1064YH19 5-PRIME, mRNA sequence.
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Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 996)
Li,W.B., Gruber,C., Jessee,J., and Polayes,D.
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BP 191 91006 EVRY cedex - France
Bmail: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
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cgi-bin/cluster.cgi7seq=CSODIO64CD100Pl&cluster=2353.r. Contact
Feng Liang Email: fllang@lifetech.com URL:
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO64CD10QP1.
Location/Qualifiers
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/note="vector: pCNVSPORT_6: lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCNVSPORT 6 vector.
Library was not normalized."
Library was not normalized: 39 others
                                                                                                                                                                                                               Contact: Genoscope

Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.ons.fr web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cg1?seq-CSODE009BE08QPlscluster=2353.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fullbagth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE009BE08QPl.

Location/Qualifiers
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                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                          1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.2%; Score 855.2; DB 13;
95.0%; Pred. No. 2.3e-218;
Live 10; Mismatches 30;
5-PRIME, mRNA sequence.
BX417429
BX417429.1 GI:30654405
                                                                        sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al Similarity 95.0%
893; Conservative
                                                                                           Homo sapiens
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primatęs;
1 (bases 1 to 1062)
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                                     BX396240.1 GI:30624830
                                                                                                                                                                                                                                                                                                                                                                                  86.5%;
llarity 99.4%;
Conservative 1
                                                       Homo sapiens (human)
Homo sapiens
                                                                                                                                Contact: Genoscope
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Matches 850; Conserv
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PORVSPORT 6 vector. Library was normalized.

192 c 248 g 256 t 18 others
                                                                                                                                         AGAGACCCTGATGCAGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
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                                                      Length
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; Pred. No. 1.9e-217;
15; Mismatches 5;
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ilarity 97.6%;
Conservative 1:
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Matches 856; Conserv
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RESULT 7 BX396240

/organism="Homo saplens"
/mol_type="mRNA"
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/dlone="cS0D1014Y109"
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/clone=lab="Homo saplens PLACENTA COT 25-NORMALIZED"
/clone="lab"-Homo saplens PLACENTA COT 25-NORMA COT 25-NO EST 13-MAY-2003 ö 327 OT 25-NORMALIZED HOMO BAPIENS CDNA 261 267 141 201 387 447 321 507 381 567 627 81 Euteleostom1; Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmall: sequefégenoscope.ons.fr. web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cg1?seq=CS0D1014AE05QPlscluster=2353.r. Contact:
freq Library Example Faraday Avenue Genoscope sequence ID: CS0D1014AE05QPl. CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTAAGACTCTG GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCTGACT ATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG **AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA** GAACTGAGAGCCATCAAACAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC 22 ATGCCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT Craniata; Vertebrata; Eutele Catarrhini; Hominidae; Homo DB 13; Length 1062; ô Indels Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization BX396240 Homo sapiens PLACENTA COT 25-NORM clone CSODI014YI09 5-PRIME, MRNA sequence. BX396240 Score 848.2; DB 13 Pred. No. 1.6e-216; 1; Mismatches 4; 382 ò 용

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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: sequef@qenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-cS0D1041BE01QP16cluster=2353.r. Contact:
Feng Lidng Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0D1041BE01QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BX358605 1076, bp mRNA 11near EST 05-MAY-2003
BX358605 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO41YI02 5-PRIME, mRNA sequence.
BX358605.1 GI:30382268
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)
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/db_xref="taxon:966"
/clone_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
 CGAAGTGTGTCTCA-TTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCA
                                                                                                                                                                                                                                                                                       681 AATTGAGGAAACC-ATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTG
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                                                      GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCTCCTTCAGGCTAAC
                                                                                                                           AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
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Homo saplens
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/tissue_type="Factoria"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSDORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
1 243 c 293 g 307 t 48 others
              AL542496 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE012Y114 5 PRIME, mRNA sequence.
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                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Emalis sequefégenoscope.ons.fr, Web : www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.ons.fr/
cg1-bin/cluster.cg1?seq-CSODE012BE07QP1scluster-2353.r. Contact :
Feng Librag Emali : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE012BE07QP1.
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98.2%; Pred. No. 7.3e-214;
tive 3; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSODE012Y114"
                                                                     AL542496
AL542496.2 GI:30547699
                                                                                                                         Homo sapiens (human)
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Contact: Genoscope
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875; Conservative
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                   VERSION
KEYWORDS
SOURCE
AL542496
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                                                                               16; Indels
                                                        Score 835.8; DB 13;
Pred. No. 3.4e-213;
4; Mismatches 16;
                                                          85.2%;
ilarity 97.4%;
Conservative
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RESULT 11 BX402751

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//organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
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/note="ist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was.
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWNSPORT 6 vector. Library was normalized."
216 c 257 g 256 t 1 others
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1007 bp mRNA linear EST 13-MAY-200. BX402751 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI084YA05 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2353.r For more information about this cluster, see thip://www.genoscope.cns.fr/cgi-bin/cluster.cgi-beg-CSIAIO2126030P1&cluster-2353.r. Contact: Feng Liang Email: fliang@lifetech.com UNL:
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Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases 1 to 1007)
Lii, W.B., Gruber, C., Jessee, J. and Polayes, D.
Luil-length obnA libraries and normalization
Unpublished
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Pred. No. 3.1e-212;
); Mismatches 3;
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99.6%;
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Query Match 84.8%; Score 831.6; DB 9; Length 1201; Best Local Similarity 95.0%; Pred. No. 4.9e-212; Matches 911; Conservative 11; Mismatches 26; Indels 11; Gaps 6; Qy 22 ATGGGACAGGTGTCTCAGGGGACTGTGCTTCCCTGGATTTGATGAGCGGCTGAT 81	Db 208 Qy 82	Oy 142 CTGTTGACATCCCGAAGTAATGCTCAGGGAAATCTCTGCAGCTTTTAAGACTCTG 2	OY 202 TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACT	Qy 262 ATTGIGGCTCTGATGAAACCCTCTGGCTTTATGATGCTGAAACATGCCTTG 321	QY 322 AAGGGAGCTGGAACAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA 381 		OY 442 GTGGTGGGGACACTTCAGGTACTACCAGCGGATGTTGGTGGTTCTCTTCAGGCTAAC 501	QY 502 AGAGACCTGATGCTGGAATTGATGATGATGATGATGATGAGAGATGTCAGGCTTTATTT 561	Qy 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAAAGTTTATCACCATCTTTGGAACA 621 	Qy 622 CGAAGIGICICATITGAGAAAGGIGITTGACAAGIACATGACTATATCAGGATITCAA 681	QY 682 ATTGAGGAACCATTGACCGGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT 741	Qy 742 GTGAAATCTATTCGAAGTATACCTGCTACCTTGCAGAGCCCTCTATTATGCTATGAAG 801	QY 802 GGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT 861	9y 862 CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGAT 921	QY 922 AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCGGGAGAAGATGA 980	RESULT 13 AL517516 LOCUS AL517516 AL517
Qy 44.2 GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC 50.1 111111111111111111111111111111111111	710 621 770	CGAAGTGTGTCTCATTTGAGAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 	Qy 682 ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT 741	Qy 742 GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTATTATGCTATGAAG 801	Oy 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGGTTTCCAGGAGTGAGATT 858	AL547761 1201 bp mRNA linear EST 31-MAX	ION AL547761 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens colone CSODIO17YJ11 5-PRIME, mRNA sequence. NA AL547761 Cortalogue		•	JOHNENT On Feb 15, 2001 this sequence version replaced gi:12882128. COMMENT Contact: Genoscope		Invitudes. Ints sequence belongs to sequence cluster 2333.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi.bin/cluster.cgi?seq=CSODIO17CE06QP1&cluster=2353.r. Contact :	reng Llang h http://full] Faraday Aver Loc	/ Adb_xref="taxon:9606"	/clone='CSUDIOIYTAII" //tissue_type="PLACENTA COT 25-NORWALIZED" //clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED" //note="lit strand CDNA was primed with a NOTI-ollogo(dT) primer. Five prime end enriched, double-strand cDNA was	digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." ORIGIN

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Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Hominidae; Homo.

E. I (bases 1 to 1201)
Eul, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12872460.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
BP 191 91006 EVRX cedex - France
BP 191 91006 EVRX cedex - France
Email: seqrefégenoscope. Cis.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODEO05DE050pl6cluster=2353.r. Contact:
Feng Liang Email: filliang@ilfetech.com URL:
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODEO06DE050Pl.
Location/Qualifiers
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                     GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGACCCTCTA-TTATGCTATGAA
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/tissue_type="PLACENTA"
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/db_xref="taxon:9606"
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/do_tref="taxon:9606"
/do_tref="taxon:9606"
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/tissue_type="NEUROBLASTOMA"
/clone="themo sapiens NEUROBLASTOMA"
/clone="themo sapiens"
/clone="
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cg1-bin/cluster.cg1?seq-cS0DA003CC03QPl&cluster=2353.r. Contact: Feng Liang Email: filang@ilfetech.com URL:
Feng Liang Email: filang@ilfetech.com URL:
Feng Avenue Genoscope sequence ID: CS0DA003CC03QPl.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                Unpublished
On Feb 13, 2001 this sequence version replaced
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotL-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                       Gaps
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; Pred. No. 1.9e-209;
18; Mismatches 29;
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94.3%;
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/clone="CSODEO04YD21"
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/clone_lib="Homo saptens PLACENTA"
/note="Vector: pCWVSPORT_6; lst strand cDNA was primed
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was normalized." 5 others
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Homo sapiens cDNA clone CSODE004YD21
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             On published
On Feb 16, 2001 this sequence version replaced gi:12952676.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgl?seq-CSODE004CBIIQP16cluster=2353.r. Contact :
Feng Liang Email: filang@iifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE004CBIIQP1.
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Li,W B., Gruber,C., Jessee,J. and Polayes,D.
Fell-length cDNA libraries and normalization
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                         ATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTC
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llarity 99.1%; Pred. No. 4.6e-209;
Conservative 5; Mismatches 1;
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/mol_type-"mRNA"
/db_xref-"taxon:9606"
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                                                                                                                                                  AL583578 Homo sapiens PLACENTA -5-PRIME, mRNA sequence.
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SUMMARIES

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Description	Modified human ann	Modified human ann	Modified human ann	Placental coagulat	Vascular anti-coad	PAP-I. Homo sapie	S65T GFP variant/h	Amino acid sequenc	Human annexin V, c
£	AAB50864	AAB50865	AAB50863	AAP80511	AAP91953	AAR13082	AAY13923	AAY84788	ABG31220
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% Query Match Length DB ID	327	327	327	320	320	320	320	320	320
Query Match	100.0	99.5	98.7	97.0	97.0	97.0	97.0	97.0	97.0
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                                  The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombior apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively reheate a radiouncilde and retain annexin bloactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.
                                                                                                                                                                                                                  ODAQALFQAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNL
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                                                                                                                                                                                          Gaps
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                                                                                                                                                                     Length 327;
extension which comprises a glycine and a cysteine residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chelation site; nuclear imaging; apoptosis;
                                                                                                                                                                                        0; Indels
                                                                                                                                                                    100.0%; Score 1639; DB 22;
100.0%; Pred. No. 9.2e-143;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                TSLYSMIKGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                          Modified human annexin, SEQ ID NO: 6.
                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB50865 standard; Proteln; 327
                  Page 33-35; 39pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2000; 2000WO-US14324
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                                                                                                                                                                  Ouery Match
Best Local Similarity 100.
Matches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown DS;
                                                                                                                                                 327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annexin;
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                  Claim 15;
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                                                                                                                                                                                                                                                          chelation site, which comprises an amino acid extension including a splicine and a cystelne residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radionuclide and retain annexin holoactivity. It can be readily prepared in high radiochemical yield and with high radiochemical purity. In distribution of conjugation chemistries that provide a chelation site remote from the site of biological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ODAQALFQAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAGGCGHMAOVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAOROEI
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                                                                                                                                                                                                                                    The present sequence is a modified annexin having an N-terminal
                                                                                                   apoptosis, has N-terminal chelation site comprising amino acid extension which comprises a glycine and a cysteine residue .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         annexin; chelation site; nuclear imaging; apoptosis;
                                                                          Novel modified annexin useful for imaging vascular thrombi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1630; DB 22;
Pred. No. 6.2e-142;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified human annexin, SEQ ID NO: 2.
                                                                                                                                                                                Claim 18; Page 37-38; 39pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 99.7
Matches 326; Conservative
2001-080465/09.
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                        N-PSDB; AAC91370
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Homo sapiens
                             EP279459-A.
JP03219875-A
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                                                                                             20-FEB-1987;
                                                                                                      23-JUL-1987;
                                                        24-AUG-1988
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                                                                                                                                             The present sequence is a modified annexin having an N-terminal chelation site, which comprises an amino acid extension including a glycine and a cysteine residue. The modified annexin is useful for imaging vascular thrombi or apoptosis which is associated with response to a chemotherapeutic agent or with rejection as a result of transplantation. The modified annexin can effectively chelate a radiouncilde and retain annexin bloactivity. It can be readily prepared in high radiochemical purity. In contrast to conventional conjugation chemistries that provide a distribution of conjugation products, the modified annexin has a single chelation site remote from the site of biological activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coagulation inhibitor; disseminated vascular coagulation;
                                                                                          Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid extension which comprises a glycine and a cysteine residue -
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                                                                                                                                                                                                                                                                                98.7%; Score 1618; DB 22; Length 327; 99.4%; Pred. No. 8e-141; 1ve 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSLYSMIKGDTSGDYKKALLLLSGEDD 327
                                                                                                                              Claim 12; Page 30-31; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Placental coagulation inhibitor.
        99US-0324096
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(updated)
(first entry)
                                                                                                                                                                                                                                                                                         Best Local Similarity 99.4 Matches 325; Conservative
                          (UNIW ) UNIV WASHINGTON
                                                              WPI; 2001-080465/09.
N-PSDB; AAC91368.
                                             Tait JF, Brown DS;
                                                                                                                                                                                                                                                               327 AA;
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10-MAR-2003
12-NOV-1990
        01-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                           This polypeptide exhibits strong anticoagulant activities and is useful for the treatment and prevention of e.g. thrombosis or disseminated intravascular coagulation in the brain, heart and peripheral blood vessels, such as cerebral and myocardial infarction. It has no antigenicity against man and can be produced in large amts. using
                                                                                                                                                                                                                                                                                  Recombinant placental coagulation inhibitor – useful for the preventior and treatment of thromboses or disseminated intra-vascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 ELRAIKOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.0%; Score 1590; DB 9;
99.7%; Pred. No. 3e-138;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP91953 standard; protein; 320 AA
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                                                                                                                                                      Suda M;
                                      87JP-0037227.
87JP-0184428.
88EP-0102468
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Matches 319; Conservative
                                                                                                                                                    Saino Y, Iwasaki A,
                                                                                                                                                                                           WPI; 1988-236733/34.
WPI; 1991-329110/45.
N-PSDB; AAN81113.
                                                                                                           (KOWA ) KOWA CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 AA;
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AAP91953
ID AAP5
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AC AAP5
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Sequence 320 AA;
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                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                    WO9109953-A
                                                                                                                   25-MAR-2003
30-SEP-1991
                                                                                                                                                                                                                                                                                                                   Foster DC;
          308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This vascular anti-coagulating protein (VAC)-alpha is used in the preparation of monoclonal antibodies (MAbs). The VAC-alpha is injected into a host animal, in conjugation with eap keyhole limper haemocyanin, and the B-cells from immunised hosts are then fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-alpha. Abs can be used as immunossay reagents to detect VAC proteins, as affinity ligands for protein purifico, and as medicaments for binding and/or neutralising VAC proteins in vivo. See also AAN91354 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
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                                                                   /ascular anti-coagulating proteins; hybridomas; B-cells; myelomas
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                                                                                                                                                                                                                                                                                                       Monoclonal antibodies to vascular anti-coagulating proteins hybridomas producing such antibodies.
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                                                                                                                  Location/Qualifiers
1..320
/product=VAC-alpha protein
                                             Vascular anti-coagulating protein-alpha.
                                                                                                                                                                                                                                                                                                                                   Disclosure; fig 1; 11pp; German.
                                                                                                                                                                                                                                     (BOEH ) BOEHRINGER INGELHEIM.
                                                                                                                                                                                               88DE-3810331
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                            (first entry)
                                                                                      - Homo sapiens
- Mus musculus
          (updated)
                    (updated)
                                                                                                                                                                                                                                                                           WPI; 1989-293724/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AA;
                                                                                                                                                                                                                                                                                      N-PSDB; AAN91353
                                                                                                                                                                                               26-MAR-1988;
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                            30-JUL-1989
                                                                                                                                                         DE3810331-A.
         25-MAR-2003
                                                                                                                                                                            05-OCT-1989
                                                                                                                                                                                                                                                          Gunther A;
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                                                                                     Chimeric
Chimeric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence, or a fragment of it, is used in the construction of hybrid phospholipid binding proteins (PBD) comprising at least one lipocortin phopholipid binding domain (PBD), e.g. of PAP-I, joined to a gla-domainless vitamin K-dependent protein, e.g. protein C or activated protein C. See AAQ12680-81 for such examples. (Updated on 25-WAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant prodn. of hybrid phospholipid-binding proteins comprising lipocortin phospholipid-binding domain and
                                                                                                                                                                                                                                                                                                                                                                                 Phopholipid; binding protein; lipocortin; domain; vitamin
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0; Mismatches
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                             KGDTSGDYKKALLLLCGEDD 320
KGDTSGDYKKALLLLSGEDD 327
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                                                                                                                                                               AAR13082 standard; Protein; 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vitamin K-dependent protein
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(first entry)
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Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC
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N-PSDB; AAQ12679.
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ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                             248 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                         QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMT1SGFQ1EETIDRETSGNLEQLLLAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
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The proteins are bifunctional Aequorea victoria green fluorescent protein composed annexin fusion proteins, where the GFP and annexin moleties provide greater or equal fluorescent intensity and anionic phospholipid binding affanity, respectively, than do the corresponding unfused GFP and annexin proteins. An early manifestation of apoptosis is the loss of the proteins. An early manifestation of apoptosis is the loss of the proteins of anionic phospholipids on the extracellular leaflet of the plasma membrane. The GFP-annexin V fusion proteins are used for the detection of apoptotic cells by flow cytometry or fluorescent microscopy. The fusion proteins provide for homogeneously labelled annexin, with fluorescence properties that do not change upon binding membrane phospholipids, unlike prior art FITC-labelled annexins, where quenching or FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid
                 248 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                  GFP; green fluorescent protein; annexin; fusion protein; apoptosis; fluorescent intensity; anionic phospholipid binding affinity; asymmetric distribution; plasma membrane phospholipid; apoptotic cell detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bifunctional fusion protein useful for the detection of apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1590; DB 20; Length 320;
Pred. No. 3e-138;
); Mismatches 1; Indels 0
                                                                                                                                                                                                                                                       S65T GFP variant/hAnnexin V protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 14-15; 23pp; English.
                                                                                                                                                               AAY13923 standard; protein; 320 AA.
                                                                           301 KGDTSGDYKKALLLLCGEDD 320
                                                           308 KGDTSGDYKKALLLLSGEDD 327
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99.78;
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                                                                                                                                                                                                                                                                                                                                                               Aequorea victoria
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                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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Annexin; phospholipid; antithrombotic; antitumor; antinflammatory; coating; thrombogenic biomaterial; labelling compound; negative charge.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemical structure having affinity for phospholipid comprises chemical platform comprising six residues supporting set of chemical functions that are capable of binding to phospholipid
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16..91
/note= "domain 1"
                                                                                                                                                                                                                                                                            AAY84788 standard; peptide; 320 AA.
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(UYPA-) UNIV CURIE PARIS VI P & M.
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308 KGDTSGDYKKALLLLSGEDD 327
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Conservative

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29-OCT-1988;
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01-NOV-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 damage to
by stroke,
                                                                                                                                                                                                                                                                                                                                                                                                Human; annexin V; delta RACK; delta protein kinase C; deltaPKC; VI domain; vasotropic; cerebroprotective; deltaV1-1; deltaV1-2; RACK; pseudo-delta receptor for activated C-kinase; deltaV1-5; PKC; protein kinase C; signal transduction; cell growth; gene expression; ion channel activity; translocation; hypoxia; stroke; ischaemic damage; creatine kinase.
                                                                                   1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLFSRSNAQRQEISAAFKTL
                                                                                                                      FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                                                                                 ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                          8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                    QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                        VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                        Gaps
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                                     Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New delta protein kinase C peptide for reducing or enhancing cells or tissues exposed to ischemic or hypoxic event caused or for protecting tissue from damage due to ischemia -
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                Human annexin V, containing a delta RACK binding site.
charges on cell surfaces and microvesicles in blood
                                                       1;
                                    DB 21;
                                    Score 1590; DB 21
Pred. No. 3e-138;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 45; Page 64-65; 65pp; English.
                                                                                                                                                                                                                                                                                                                          ABG31220 standard; Protein; 320 AA
                                                                                                                                                                                                                                                                      KGDTSGDYKKALLLLSGEDD 327
                                     97.0%;
                                             99.78;
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                                             Best Local Similarity 99.7
Matches 319; Conservative
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                   320 AA;
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derivatives or fragments. Protein Kinase C (PKC) is a key enzyme in signal transduction involved in a variety of cellular functions including cell growth, regulation of gene expression and ion channel activity. The coll growth, regulation of different PKC isozymes to different areas of the cell in turn appears due to binding of the activated isozymes to the specific anchoring molecules (RACKS). Peptides that miller either the PKC-binding site on RACKS or the RACK binding site on PKC are isozyme specific translocation inhibitors of PKC. The disclosed peptides are useful in activating or inhibiting translocation or function of deltaPKC. The deltaPKC agonists or antagonists are useful in reducing, enhancing or protecting against damage to cells or tissues due to ischaemic or hypoxic event caused by stroke. Acute administration of the peptides, conjugated to a carrier peptide or a Tat-derived peptide, protected hearts against ischaemic damage as shown by decreased release of creatine kinase. The data indicate that in an intext heart, inhibition of deltaPKC conferred greater than 50% protection against ischaemic damage. The sequence presented is human annexin V, which contains a delta RACK binding site.
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deltaV1-5 or their
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FGRDLLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEITASRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELRAIKOVYEEEYGSSLEDDVVGDTSGYYORMLVVLLQANRDPDAGIDEAQVEQDAQALF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
   pseudo-delta receptors for activated C-kinase (RACK),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.0%; Score 1590; DB 23; 99.7%; Pred. No. 3e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3e-138;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anticoagulant; PP4 protein; thromboplastin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGDTSGDYKKALLLLSGEDD
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Best Local Similarity 99.7
Matches 319; Conservative
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N-PSDB; AAA11241
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13-NOV-1990
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                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carrier; thrombus; thrombolytic; fusion protein; fibrinolysis.
                                                                                                                                                                                                   8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                            ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                             OAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                    ö
                                                                                                                                                                   Length 320;
                                              and new recombinant protein, vectors, antibodies, etc., useful therapeutically and diagnostically.
                                                                                                                                                                                    Indels
                                                                                                Amino acid sequence of anticoagulant PP4 protein. This inhibits blood coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                 96.8%; Score 1587; DB 10; 99.4%; Pred. No. 5.6e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
                                                                                                                                                                                   1; Mismatches
                                                                                 Claim 1; page 11 and Table 1; 12pp; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Annexin V/urokinase fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                 AAY92930 standard; Protein; 600
                 Kupper
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                                                                                                                                                                         Best Local Similarity 99.4
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thrombocyte;
insect cell;
(BEHW ) BEHRINGWERKE
                                WPI; 1989-166767/23
                                                                                                                                                  320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Annexin V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             urokinase;
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                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248, VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL

    comprises

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                                                                                                                                                                                                                                                                                                                                                                           96.8%; Score 1587; DB 21; Length 600; 99.4%; Pred. No. 1.4e-137; ive 1; Mismatches 1; Indels · 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAP-I isolated from biological fluid, used as anticoagulant.
                                                                                         New thrombolytic fusion protein for targetting thrombus fusion of Annexin V and urokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 2-4; 20pp; Chinese.
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(first entry)
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Matches 318; Conservative
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                                   WPI; 2000-413098/36.
Sun J, Yang
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319 AA;
      JP04198195-A
                                                                                    28-NOV-1990;
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                                            17-JUL-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL 67
                                                                                                                                                                                                                         Human proteins having anticoagulant and antiinflammatory activity - . isolated from biological fluid by anion-exchange chromatographoc media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                     The protein does not contain a leader peptide sequence, indicating that PAP-I is probably not constitutively secreted. The Met residue is removed at in a post-translational event and the newly formed NH2-terminal Ala residue is blocked by acetylation. It binds to phospholipid and inhibits phopholipase A2. The protein can substitute heparin or other anticoagulants in the treatment of disseminated intravaccular coagulation, deep vein thrombosis, or other disorders. It also has antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1586; DB 9; Length 3
Pred. No. 6.9e-138;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                        Carter BLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR26276 standard; protein; 319 AA
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                                                                                                                                                                                                                                                                                   Disclosure; Page ?; ?pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.8%;
87US-0011782
87US-0059355
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(first entry)
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Matches 318; Conservative
                                                             (ZYMO ) ZYMOGENETICS INC.
                                                                             UNIV WASHINGTON
                                                                                                                        Fujikawa K, Irani MH,
                                                                                                                                                           WPI; 1988-235049/33.
N-PSDB; AAN82107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                320 AA;
06-FEB-1987;
05-JUN-1987;
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04-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                              The sequence given is the amino acid sequence of CPB-I. CPB-I was used within a method which involved adding basic amino acids to it which resulted in its stabilisation. This lead to the production of CPB-I which keeps is activity when it is frozen, molten or has been processed by several procedures. (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 319;
                                                                                                                                                                                                                                                                  Stabilisation of CPB-1 for drug compsn. - by adding basic aminoacid selected from lysine, arginine and/or ornithine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.7%; Score 1585; DB 13;
99.7%; Pred. No. 8.5e-138;
11ve 0; Mismatches 1;
                                                                                                                      (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
(KOWA ) KOWA CO LTD.
                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 2; 4pp; Japanese
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90JP-0328286
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26-FEB-2001; 2001JP-0050297
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
calcium/phospholipid binding protein; polyhydric alcohol.
                                                                                                                                                                         intravenously, orally, intramuscularly, percutaneously or rectally
                                                                                                                                             of
1s
                                                                                                                                   Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I) inhibits protein kinase C (PKC) and is useful in the treatment amalignant tumours caused by abnormal activation of PKC. CPB-I extracted from human or animal organs and may be applied
                                                                                       Protein kinase C inhibitor effective against malignant tumours contg. (opt. recombinant) calphobindin I
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Pred. No. 8.5e-138;
0; Mismatches 1; Indels 0
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                                                                                                                   Claim 1; Page 2-3; 6pp; Japanese
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       92JP-0019032
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                                                                                                                                                                                                                                                                             The invention relates to eye drops contain CPB-1 (anexin V) and a polyhydric alcohol having a carbonyl value of not more than 5micro Mol./g. The eyes drops are for treating e.g. corneal diseases. Such eye drops are without unpleasant irritation upon dropping but wi satisfactory long-term storage stability. The present sequence is the human CPB-1 (calcium/phospholipid binding) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                              Eye drops for treating e.g. corneal diseases, contain CPB-I and polyhydric alcohol with specific carbonyl value, without unpleasant irritation upon dropping but with satisfactory long-term storability
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Pred. No. 8.5e-138;
); Mismatches 1;
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(KOWA ) KOWA CO LTD.
(KAGA ) CHEMO-SERO-THERAPEUTIC
                                                            Shinoda Y,
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99.78;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 22, 2003, 21:30:17 ; Search time 15 Seconds Run on:

(without alignments) 2096.477 Million cell updates/sec

Perfect score: Sequence:

US-09-970-969-4 1639 1 MAGGCGHWAQVLRGTVTDFP......KGDTSGDYKKALLLLSGEDD 327

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% 'Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

	Description	annexin V [validat	>	>	>	\I	ΙΛ	annexin IV - human	annexin IV - piq	annexin VI - rat	annexin IV - bovin	annexin - chicken	×	annexin XI form B	annexin XI - rabbi	annexin XI - human	annexin VIII - hum	annexin III - huma	annexin VII, long	annexin III - rat	annexin VII - mous	annexin XII - Hydr	ı	hypothetical prote		annexin II - bovin	annexin II - rat	annexin II - mouse	annexin II - rat	annexin IX - fruit
SUMMARIES	ID	AQHUP	S27214	LURTS	LUCHS	AQHU68	S01786	A42077	LUPG4	S52844	LUBO4	JC2029	LUBO11	S23447	LURB11	A53152	LUHU8	LUHU3	LUHU7	LURT3	S29170	LUJF12	S70644	S41022	LUHU36	LUBO36	833700	LUMS36	S55277	LUFF9
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	Query	97.0	93.7	88.8	78.0	56.9	56.9	56.3	26.2	56.2	55.8	54.7	52.8	52.8	52.7	52.2	50.7	49.0	47.5	47.3	٠	43.8	43.4	43.3	42.6	42.4	42.3	42.5	41.6	41.6
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annexin XIII, inte														
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30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

_	RESULT 1
	AQHUP
	annexin V [validated] - human
	N; Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; place
_	C; Species: Homo sapiens (man)
	C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Dec-2000
	C; Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C31953; S06646;
	R; Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Brownin
	J. Biol. Chem. 263, 10799-10811, 1988
	A; Title: Five distinct calcium and phospholipid binding proteins share homology with
	A; Reference number: A92659; MUID:88273202; PMID:2968983
	A; Accession: D29250
	A; Molecule type: mRNA
	A; Residues: 1-320 <pep></pep>
-	A CONTRACT OF CONTRACT CONTRAC

"....uss-reterences: GB:M21731; NID:g186969; PIDN:AAA36166.1; PID:g307116
R;Grundmann, U.; Abel, K.J.; Bohn, H.; Loebermann, H.; Lottspeich, F.; Kuepper, H.
Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988
A;Title: Characterization of cDNA encoding human placental anticoagulant protein (PP4
A;Aritle: Characterization of cDNA encoding human placental anticoagulant protein (PP4
A;Accession: A30206
A;Acce

A; Keaplan, R.; Jave, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.
J. Biol. Chem. 263, 8037-8043, 1988
A; Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+) and phosphol A; Reference number: A28076; MUID:88228020; PMID:2967291
A; Accession: A28076
A; Molecule type: mRNA
A; Residues: 1-320 < KAP>
A; Cross-references: GB:J03745; NID:9182111; PIDN:AAA52386.1; PID:9182112
B; Maulecule type: mRNA
A; Residues: 1-320 < KAP>
A; Cross-references: GB:J03745; NID:9182111; PIDN:AAA52386.1; PID:9182112
B; Maulecule type: mRNA
A; Residues: 1-320 < KAP>
A; Cross-reference number: S01016; MUID:88271329; PMID:2455636
A; Ricerence number: S01016; MUID:88271329; PMID:2455636
A; Recession: S01016
A; Molecule type: mRNA
A; Residues: 1-320 < KABD>
A; Cross-references: EMBL:X12454; NID:937636; PIDN:CAA30985.1; PID:937637
A; Note: part of this sequence was confirmed by protein sequencing
B; Funakoshi, T.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
B; Roderence number: A29417; MUID:88164463; PMID:2964863
A; Cross-references: EMBL:X12454; NID:98164463; PMID:2964863
A; Cross-references: EMBL:X12454; NID:98164463; PMID:2964863
A; Cross-references: EMBL:X12454; NID:98164463; PMID:2964863

A; Accession: A29417 A; Molecule type: mRNA A; Residues: 1-320 <FUN>

A;Cross-references: EMBL:M18366; NID:g179131; PIDN:AAA35570.1; PID:g179132 R;Iwasaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saino, Y.; Arai, K.; Mizoguchi, T.; S P. Bicchem. 102, 1261-1273, 1987 A;Title: Structure and expression of cDNA for an inhibitor of blood coagulation isola

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Score 1590;
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Matches 319, Conservative
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A;Residues: 1-320 <LEA>
A;Accession: S27215
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A; Map position: 4426-4428
A; Map position: 4426-4428
A; Introns: 3,3,32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
A; Introns: 3,3,32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3
C; Superfamily: annexin I; annexin repeat homology
C; Keywords: acetylated amino end; anticoagulant: cancium binding; duplication; endonexin F; 2-320/Product: annexin repeat homology <AX2>
F; 18-89/Domain: annexin repeat homology <AX2>
F; 10-151/Pomain: annexin repeat homology <AX2>
F; 10-151/Pomain: annexin repeat homology <AX3>
F; 185-201/Region: endonexin fold %status predicted
F; 173-245/Domain: annexin repeat homology <AX3>
F; 185-201/Region: endonexin fold %status predicted
F; 245/Domain: annexin repeat homology <AX3>
F; 186-201/Region: endonexin fold %status predicted
F; 245/Pomain: annexin repeat homology <AX3>
F; 186-210/Pomain: annexin repeat homology <AX3>
F; 186-210/Pomain: annexin repeat homology <AX3>
F; 260-276/Region: endonexin fold %status predicted
F; 240/Modified site: acetylated amino end (Ala) (in mature form) %status experimental
F; 23/Rinding site: phosphate (Thr) (covalent) %status predicted
F; 28/30,32,72/Binding site: calcium, high affinity (Met, Gly, Glu) %status experime
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FEBS Lett. 275, 15-21, 1990
A; Title: The calcium binding sites in human annexin V by crystal structure analysis at 2 A; Tochents: annotation: X-ray crystallography, 2.0 angstroms
A; Reference number: A37250; MUID:91085549; PMID:2148156
A; Contents: annotation: X-ray crystallography, 2.0 angstroms
A; Note: three calcium ions are strongly bound at sites in the first, second, and fourth R; Funakoshi, T.; Heimark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.
Biochemistry 26, 5572-5578, 1987
A; Title: Human placentral anticoagulant protein: isolation and characterization.
A; Reference number: A29670; MUID:88050845; PMID:2960376
A; Accession: A29670
A; Morgan, R.O.; Fernandez, M.R.; Carcedo, M.T.
Gene 149, 253-256, 1994
A; Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C cont A; Reference number: 137172; MUID:9504784; PMID:7958998
A; Accession: 137172
A; Residues: 1-320 < RES
A; Rosidues: 1-320 < RES
A; Cross-references: EMBL:001691; NID:9430964; PIDN:AAB40047.1; PID:9430966
A; Cromment: Annexins undergo reversible, calcium-dependent binding to membrane phospholify
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A;Residues: 85-93 <AHN>
R;Rothhut, B.; Comera, C.; Cortial, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; Cd
Biochem. J. 263, 929-935, 1989
A;Title: A 32 KDa lipocortin from human mononuclear cells appears to be identical with t
A;Reference number: S06646; MUID:90088443; PMID:2532007
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A; Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>
A; Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>
B; Ahn, N.G.; Teiller, D.C.; Bienkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.
J. Biol. Chem. 263, 18657-18663, 1988
A; Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-;
                                                                                                                                                                                                                                                                                                                                          calcium- and
        A; Molecule type: mRNA
A; Residues: 1-320 CIMA>
A; Cross-references: GB: D00172; NID: 9219480; PIDN: BAA00122.1; PID: 9219481
A; Note: part of this sequence was confirmed by protein sequencing
R; Schlaepfer, D.D.; Mehlman, T.; Burgess, W.H.; Halgler, H.T.
Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6087
A; Title: Structural and functional characterization of endonexin II, a ca
A; Reference number: A28038; MUID: 87317598; PMID: 2957692
A; Molecusin. A28038
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A; Accession: C31953
A; Reference number: A41514; MUID:88139278; PMID:2963810
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C. Superfamily: annexin velve themology control in the inhibition of blood coage olipid-binding rather than proteolytic inactivation. It does not affect thrombin-deper C. Superfamily: annexin repeat homology

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A;Residues: 1-35, T, 37-124, E, 126-320 <LE2>
Note: It is uncertain whether the sequence differences are due to allelic variation
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho
                                                                                                                                                               (Leu, Gly, Gly, Asp) #status
(Met, Gly, Gly, Asp) #status
F;33,35,36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status experimental F;73,78/Binding site: calcium, low affinity (Leu, Glu) #status experimental F;100,102,104,144/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp) #status F;259,261,263,303/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELRAIKOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
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0; Mismatches 1
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A; Contents: erratum
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C;Genetics:
A;Introns: 1/3; 30/1; 61/3; 99/3; 130/1; 156/3; 175/3; 207/1; 239/1; 258/3; 299/3
C;Superfamily: annexin I; annexin repeat homology
C;Reywords: calcium binding; duplication; endonexin fold; membrane-associated protein; proceed cynomics: calcium binding; duplication; endonexin fold; membrane associated protein; proceed cynomics: calcium binding; duplication; endonexin prepart homology caxis
F;16-87/Domain: annexin repeat homology caxis
F;18-43/Region: endonexin fold #status predicted
F;171-243/Domain: annexin repeat homology caxis
F;181-199/Region: endonexin fold #status predicted
F;27-318/Domain: annexin repeat homology caxis
F;28-319/Region: endonexin fold #status predicted
F;26,28,30,70/Binding site: calcium, high affinity (Met, Glu, Asp) #status predicted
F;31,33,34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status predicted
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C; Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
A; Accession: C20250; S6680
B; Pepinsky, R.B.; Tizard, R.; Mattaliano, R.J.; Sinclair, L.K.; Miller, G.T.; Browning, J. Biol. Chem. 263, 10799-10811, 1988
A; Title: Five distinct calcium and phospholipid binding proteins share homology with lip A; Reference number: A92659; MUID:88273202; PMID:2968983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annexin V - rat
N;Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; placenta
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C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
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                                                                                                                                                                                                                                                                              GROLLDOLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
                                                                                                                                                                                                                                                                                                                                           AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV 248
                                                                                                                                                                                                                                                                                                                                                                                                                             KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK 308
                                                                                                           AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                Gaps
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A;Residues: 1-319 <PEP>
A;Cross-references: GB:M21730; NID:g205138; PIDN:AAA41512.1; PID:g205139
        Length 320;
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.5; DB 1;
1.1e-91;
hes 5;
    Score 1536.5;
Pred. No. 1.1e-
5; Mismatches
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    93.7%;
96.6%;
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                        Local Similarity
nes 309; Conserv
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Best Local S
Matches 309
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A;Accession: S32523
A;Status: prellminary
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 6-20;B5, X', 87-88, 'X', 90-93, 'X', 95-96, 'XX', 99-100, 'X', 102-103, 'XX', 106-10
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho
F:71,76/Binding site: calcium, low affinity (Leu, Glu) #status predicted F:98,100,102,142/Binding site: calcium, high affinity (Leu, Gly, Gly, Asp) #status pr F:257,259,261,301/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status p
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A; Residues: 1-118, 'LLKCRILNRFINNOEYEANLGRNKITGRRHQAIFRDCWWSCCRQIEI', 163-167, 'E', 169-32
A; Cross-references: GB: M30971; GB: J03194; NID: g211138
B; Genge, B.R.; Wu, L.N.Y.; Adkisson IV, H.D.; Wuthler, R.E.
J. Biol. Chem. 266, 10678-10685, 1991
A; Title: Matrix vesicle annexins exhibit proteolipid-like properties. Selective parti
A; Reference number: A40404; MUID: 91244852; PMID: 2037607
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A; Residues: 188-199 (GEDN)
A; Residues: 188-199 (GEDN)
A; Residues: 188-199 (GEDN)
B; Walker, J.H.
B; Boustead, C.M.; Brown, R.; Walker, J.H.
Biochem, J. 291, 601-608, 1993
A; Title: Isolation, characterization and localization of annexin V from chicken liver
A; Reference number: 332523; MUID:93249384; PMID:8484740
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C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1992 **sequence_revision 30-Sep-1992 *text_change 02-Jun-2000
C;Accession: A35381; A28623; B40404; S32523; S08771
R;Fernandez, M.P.; Selmin, O.; Martin, G.R.; Yamada, Y.; Pfaeffle, M.; Deutzmann, R.; J. Biol. Chem. 265, 8344, 1990
A;Reference number: A35381; MUID:90243721; PMID:2159478
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                                                                                                                                                                                                                                                                                                       12 LRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA
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                                                                                                                                                         DB 1; Length 319;
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                                                                                                                                                 Query Match 88.8%; Score 1455.5; DB 1; Best Local Similarity 91.8%; Pred. No. 1.8e-86; Matches 291; Conservative 12; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 SGDYKKALLLL-SGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA A; Residues: 1-321 <FER>
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us-09-970-969-4.rpr

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A. Molecule type: mRNA
A. Residues: 1-225, WK', 228-554, T', 556-673 <SUE>
A. Molecule type: mRNA
A. Residues: 1-225, WK', 228-554, T', 556-673 <SUE>
A. Crosa-references: GB:103578; NID:g179975; PIDN:AA35656.1; PID:g179976
B. Yoshizaki, H.; Mizoguchi, T.; Arai, K.; Shiratsuchi, M.; Shidara, Y.; Maki, M.
J. Blochem. 107, 43-50, 1990
A. Aritile: Structure and properties of calphobindin II, an anticoagulant protein from h
A. Reference number: JX0091; MUID:90236978; PMID:2139657
A. Molecule type: protein
A. Molecule type: protein
A. Residues: 2-299,307-314,320-445,447-549;581-673 <YOS>
B. Residues: 2-299,307-314,320-445,447-549;581-673 <YOS>
A. Molecule type: protein
A. Residues: 2-299,307-314,320-445,447-549;581-673 <YOS>
A. Molecule type: A. M. R.; Sonobe, S.; Kakunaga, T.
J. Biol. Chem. 264, 1722-17330, 1989
A. Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding prot
A. Reference number: A34459; MUID:90008880; PMID:2529258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. Accession: B31953
A. Molecule type: protein
A. Residues: 90-1089, L., 110-126,127,265-276;286-302;626-654 <AHN>
A. Residues: 90-1089, L., 110-126,127,265-276;286-302;626-654 <AHN>
B. Hyatt, S. L.; Liao, L.; Chapline, C.; Jaken, S.
Blochemistry 33, 1223-1228, 1994
A. Title: Identification and characterization of alpha-protein kinase C binding protein
A. Reference number: A33507; MUID:94153907; PMID:8110754
A. Molecule type: protein
binds to the inner surface of the cell mem
A; Molecule type: protein
A; Rolecule type: protein
A; Residues: 103-113;167-172, 'x', 174-177;232-235, 'F', 237-240;251-258;277-281;359-362,'
A; Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-
A; Note: eight calculum ions are bound in the presence of phospholipid
B; Suedhof, T.C.; Slaughter, C.A.; Leznicki, I.; Barjon, P.; Reynolds, G.A.
Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988
A;Title: Human 67-kDa calelectrin contains a duplication of four repeats found in 35-
A; Reference number: A31079; MUID:88124902; PMID:2963335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Experimental source: placenta
R;Ahn, NG.; Teller, D.C.; Blankowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C
J. Biol. Chem. 263, 18657-18663, 1988
A;Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 10-25;69-75;136-151;192-207;209-220;300-306 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A92696; MUID:89066652; PMID:2974032
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A; Map position: 5q22-5q34
C; Superfamily: annexin repeat homology
C; Keywords: acetylated amino end; calcium binding; dup;
F; 2-673/Product: annexin VI **status experimental cMaT>
F; 23-64/Domain: annexin repeat homology cAXI>
F; 34-50/Region: endonexin fold **status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95-166/Domain: annexin repeat homology <AX2>
106-122/Region: endonexin fold #status predicted
178-250/Nomain: annexin repeat homology <AX3>
178-250/Region: endonexin fold #status predicted
1254-325/Domain: annexin repeat homology <AX4>
1255-281/Region: endonexin fold #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #status predicted homology <AX5>
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58.1%;
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:449-465/Region: endonexin fold
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Best Local Similarity 58.13
Matches 183; Conservative
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F; 366-437/Domain:
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                         Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula clipid-binding rather than proteolytic inactivation. It does not affect thrombin-depended cosputerfamily: annexin is annexin is more peat homology (C. Superfamily: annexin is annexin repeat homology (C. Superfamily: annexin repeat homolo
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A;Molecule type: mRNA
A;Residues: 1-673 <IMAA
A;Cross-references: EMBL:D00510; NID:g219550; FIDN:BAA00400.1; PID:g219551
A;Cross-references: EMBL:D00510; NID:g219550; FIDN:BAA00400.1; PID:g219551
EMBO J. 7, 21-27, 1988
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C;Species: 11.Mar.1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
C;Accession: J100032; S00263; S18519; A31079; JX0091; B34459; B31953; A53507
R;Iwasaki, A.; Suda, M.; Watanabe, M.; Nakao, H.; Hattori, Y.; Nagoya, T.; Saino, Y.; J. Blochem. 106, 43-49, 1989
A;Tille: Structure and expression of cDNA for calphobindin II, a human placental coaguA;Reference number: J100032; MUID:89380132; PMID:2528541
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A;Residues: 1-616, D',620-673 <CR1>
A;Cross-references: EMBL:X00097; NID:935217; PIDN:CAA68286.1; PID:935218
A;Accession: S18519
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Matches 250; Conservative
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mature form) #status experimental ö Gaps Length 673 Indels Score 932; DB 1; Pred. No. 2.1e-52; predicted F; 2/Modified site: acetylated amino end (Ala) (in homology <AX8>

duplication; endonexin fold; phosp

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A. Molecule type: DNA
A. Residues: 87-129 cTAZ>
A. Reference number: 59-67, 1988
A. Title: Isolation and expression of cDNA coding for a new member of the phospholipas
A. Reference number: 507434; MUID: 88309022; PMID: 2970257
A. Reference number: 507434
A. Reference number: 507434
A. Residues: preliminary
A. Molecule type: mRNA
A. Residues: 1-97, 0′, 99-321 cGRU>
A. Cross-references: EMBL: MJ9383; NID: 9189616; PIDN: AAC41689.1; PID: 9189617
B. Cross-references: EMBL: MJ9383; NID: 9188654
A. Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 29-58; IOI - 126; 282-310 < AHN>
A; Residues: 29-58; IOI - 126; 282-310 < AHN>
R; Tait, J.F.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E
Blochemistry 27, 6268-6276, 1988
A; Title: Placental anticoagulant proteins: isolation and comparative characterization
A; Title: Placental anticoagulant proteins: isolation and comparative characterization
A; Reference number: A90534; MUID:89118212; PMID:2975506
A; Accession: A31046
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C; Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; glyco
C; Keywords: acetylated amino end; calcium binding;
E; 2-321/Product: annexin IV #status predicted <MAT>
E; 19-90/Domain: annexin repeat homology <AXI>
E; 30-46/Region: endonexin fold #status predicted
E; 91-62/Domain: annexin repeat homology <AX2>
E; 103-118/Region: endonexin fold #status predicted
E; 174-246/Domain: annexin repeat homology <AX3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.A.; Disteche, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N; Alternate names: endonexin I; placental anticoagulant protein II; PP4-X protein
                                                                       252
                                                                                                                                                                                                   STPEYFAERLEKAMKGLGTRDNTLIRIMVSRSELDMLDIREIFRTKYEKSLYSMIKNDTS 310
                                                                                                                                                                                                                                                                                    SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Homo sapiens (man)
C; Date: 30-Jan-1993 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C; Accession: A42077; B42077; S07434; A31953; A31046
G; Accession: A42077; March C; Frankenberry, D.A.; Miao, C.H.; Adler, D.A.; Distection of the human annexin IV (ANX4) gene.
A; Title: Cirromosomal mapping of the human annexin IV (ANX4) gene.
A; Reference number: A42077; MUID:92155721; PMID:1346776
                                                                                                                                                               KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                          KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-321 <TAL>
A;Cross-references: GB:M82809; NID:g178698; PIDN:AAA51740.1; PID:g178699
A;Accession: B42077
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A;Map position: 2p13-2p13
A;Introns: 102/3
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A; Residues: 4-17;30-74;102-146;283-321
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311 GEYKKALLKLCGGDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                   GDYKKALLLLSGEDD 327
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N.Alternate names: calcium-binding protein p68; calelectrin; calphobindin II
C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1889 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C.Accession: S01786
C.Date: 30-Sep-1889 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C.Accession: S01786
R.Hoss, S.E.; Crompton, M.R.; Crumpton, M.J.
Eur. 1 Biochem. 177, 21-27, 1988
A.Title: Molecular cloning of murine p68, a Ca-binding protein of the lipocortin family.
A.Accession: S01786; MUD:89030687; PMID:2972541
A.Accession: S01786; MUD:89030687; PMID:2972541
A.Accession: S01786; MUD:89030687; PMID:2972541
A.Accession: S01786
A.Holecular cloning of murine p68, a Ca-binding protein of the limer surface of the cell membra A:Residues: 1-673 accossore Embi.xia460; NID:89030687; PMID:2972541
A.Accession: S01786
A.Ac
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                                                                                                                              133 KQYYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                    190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
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                                   70
KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                               13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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C.Species: Rattus norvegicus (Norway rat)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: S65683; S55683; S5583; S55883; Specific regulation of expression of rat calcium-bin A; Reference number: S65683; MUID:95331313; PMID:7607247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endonexin fold; membrane-associate
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                                                                                                                                                                                                                                                                                                                                                      253
                                                                              193
                                                                                                                                                                                                                                                      254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304
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              GTVKAASGFNAAEDAQTLRKAMKGLGTDEDAIISVLAYRSTAQRQEIRTAYKSTIGRDLL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
                                                                                                                                                                                                                                                                                                                                                      WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
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A;Residues: 1-673 <PAN>
A;Cross-references: EMBL:X86086; NID:9763180; PIDN:CAA60040.1; PID:9763181
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58.7%; Pred. No. 1e-51;
tive 48; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Experimental source: liver
C. Superfamily: annexin VI; annexin repeat homology
C. Superfamily: annexin VI; annexin repeat homology
F. Sey-Vorduct: acetylated amino end; calcium binding;
F. 2-67-Product: annexin VI #status predicted «MAT>
F. 23-94-Domain: annexin repeat homology «AXI>
F. 95-166-Domain: annexin repeat homology «AXI>
F. 95-166-Domain: annexin repeat homology AXI>
F. 106-122/Region: endonexin fold #status predicted
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F:538-554/Region: endonexin fold #status predicted
F:602-673/Domain: annexin repeat homology <AX8>
F:613-629/Region: endonexin fold #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:| ||:| || || DYRKVLLILCGGDD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYKKALLLLSGEDD 327
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Best Local Similarity 58.7%
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;438-509/Domain: annexin
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C. Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoproteil
Fib.6.**J/Domain: annexin repeat homology <AXI>
Fib.6.**J/Domain: annexin repeat homology <AXI>
Fib.17.**Pegion: endonexin fold *status predicted
F: 89-115.**Region: endonexin fold *status predicted
F: 8171-243.**Domain: annexin repeat homology <AXI>
Fil.8.**J.99.**Region: endonexin fold *status predicted
F: 1747-318.**Domain: annexin repeat homology <AXI>
F: 183-199.**Region: endonexin fold *status predicted
F: 258-274.**Region: endonexin fold *status predicted
F: 248-318.***Covalent) (by protein kinase C) *status predicted
F: 248-318.***Covalent) (covalent) *status predicted
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A;Residues: 1-318 <WEB>
A;Experimental source: intestinal epithellum
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phosphollp
F;186-202/Region: endonexin fold #status predicted
F;250-321/Domain: annexin repeat homology <AX4>
F;251-277/Region: endonexin fold #status predicted
F;261-277/Region: endonexin fold #status predicted
F;27/Modified site: acetylated amino end (Ala) (in mature form) #status predicted
F;9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;247/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                   14 GTVTDPPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                          GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
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                                                                                                                                                                                                                                           / Match 56.3%; Score 923; DB 1; Length 321; Local Similarity 58.3%; Pred. No. 3.1e-52; nes 183; Conservative 53; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:| ||:| || || DYRKVLLVLCGGDD 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 58.6
tes 184; Conservative
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Best Local S
Matches 183
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:: :: ::	Qy 74 DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
QY 193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252	DD 66 DDLKSELSGNPBQVILGMMTPTVLYDVQELRKAMKGAGTDEGCLIEILASRTPEEIRRIN 125
AGFIYILGNRSKQHLRLVFDEYLKTTGKPIEASIRGELSGDE	Qy 134 QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK 193
OY 253 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLENIRKEFRKNFATSLYSMIKGDTS 312	RSLEDDIRSDTSFMFORVLVSLSAGGRDESNYLDDALMRQDAQI
Db 251 STPEYFAERLFKAMKGLGTRDNTLIRIMVSRSELDMLDIREIFRTKYEKSLYSMIKNDTS 310 Qy 313 GDYKKALLLLSGEDD 327	OY 194 WGTDEEKFITIFGTRSVSHLRKVFDKYWTISGFOIEETIDRETSGNLEQLLLAVVKSIRS 253
:	254 IPAXLAETLYXAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
ç	246 KSAYFAERLYKSMKGLGTDDDTLIRVMVSRAEIDMLDIRANFKRLYGKSLYSFIKGDTSG
annexin IV - bovine N.Alternate names: 32K calelectrin; chromobindin IV; endonexin; lipocortin IV; protein I	
C;Species: Bos prinigenius taurus (cattle) C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999 C;Accession: A31578; D45066; S59624; A45066; B45066; C45066; G45066; H45066	RESERT 11
	 n - chicken
A:Title: Cloning and characterization of a cDNA encoding bovine endonexin (chromobindin A:Reference number: A31578; MUID:89050088; PMID:2847715	N;Alternate names: 67K lipid-dependent Ca2+-binding protein C;Species: Gallus gallus (chicken)
A.Accesion: A31578 A.Molecule Type: mRNA	nge 17-Mar-1
A; McBiddes: 1-319 CHAM> A; McBiddes: 1-319 CH	M.; Wuthier, R.E.
Marsumo	A/TILLE: Characterization, cloning and expression of the 6/-kDa annexin from chicken A/Reference number: JC2029; MUID:94092130; PMID:8267590
A;III.E: Carbonydrate-binding proteins in bowine Kidney have consensus amino acid sequen A;Berence number: A45066; MUID:93015942; PMID:1400371 A:Bereseive: D45066	A; Accession: JC2029 A; Molecule type: mRNA
A; Molecule 19,000 A; Molecule 19,00: protein A: Desidines: 10,10 (v/)0.23 (v/)0.25.30.40.101.107 (v/)00.110.(v/)01.107 (v/)00.00 (v/)00.	A; Residues: 1-6/1 <cao> C; Superfamily: annexin repeat homology</cao>
Restudes: 10-10, A , Z0-Z2, A , Z4-Z3,Z9-40;IUI-IU/, A ,IU9-II0; A ,I94-I9/ Experimental source: kidney	C;KeyWords: calcium binding; phospholipid binding F;21-92/Domain: annexin repeat homology <ax1></ax1>
A:NOTE: Sequence extracted from NCBI backbone (NCBIP:116211, NCBIP:116208, NCBIP:116209, A:NOTE: these fragments are derived from a 33K protein that exhibited Ca++-dependent bid	F;93-164/Domain: annexin repeat homology <ax2> F;176-248/Domain: annexin repeat homology <ax3></ax3></ax2>
Sohma,	F;252-323/Domain: annexin repeat homology <ax4> F;364-435/Domain: annexin repeat homology <ax5></ax5></ax4>
BIOCNEM. J. 311, 1/7-181, 1995 A.Title: Caf.dependent binding of annexin IV to surfactant protein A and lamellar bod A.Reference number: SSG674. WITD:06077140: DWID:7409310	F.436-507/Domain: annexin repeat homology <ax6> F.525-597/Domain: annexin repeat homology <ax7> F.505-597/Domain: annexin repeat homology <ax7> F.601-671 Averages</ax7></ax7></ax6>
A) Accession: S59624	
A;Suclus: preliminary A;Molecule type: protein A:Residies: 20-44:72-77-112-119-163-181-190:226-235 /coux	Query Match Query Match S4.7%; Score B96.5; DB 2; Length 671; Best Local Similarity 57.7%; Pred No. 3.9e-50; Best Local Similarity 57.7%; Pred No. 3.9e-50; Best 104. Occornation 51. Witnestons 03. Todols 1. Cans 1.
C; Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip	FRACCISCS 104, COLDECTACTIVE 51, MIDDRECHES 65, INCRES 1, GAPS 10 ANTERPRESENTADOS DA ANTERIOR MANAGEMENT TO GENERAL PRINCES CANADA DE C
C;Superfamily: annexin I; annexin repeat homology C;Reywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin	OY TO COLORIA TO ESTABLISH THE TOTAL TO THE TOTAL ESTABLISH THE TOTAL OF THE TOTAL ESTABLISH THE TOTAL OF THE TOTAL ESTABLISH THE TOTAL OF THE TOTAL
F:2-319/Product: annexin IV #status predicted <mat> F:17-88/Domain: annexin repeat homology <axi> F:38-44/Remion: endonexin fold #starus predicted</axi></mat>	OY 70 RDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEWVLTEITASRTPEEL 129
F:89-160/Domain: encourant for the state of	Db 66 KDLIADLKYELTGKFERLIVSLMRPPAYSDAKEIKDAIAGIGTDEKCLIEILASRTNQEI 125
F.172-244/Domain: annexin repeat homology AXX3>	ANRDPDAGIDEAOV
Filey-low, region: encouexin lord #sterus predicted F/2540-319/Domain: ennexin repeat homogy <ax4> F/2540-275/Redion: endomevin fold #status predicted</ax4>	Db 126 HDLVAAYKDAYERDLEADVVGDTSGHFRKMLVVLLQGAREEDDVVSEDLVEQDARDLLEA 185
F:7/Blnding site: phosphate (Thr) (covalent) (by protein kinase C) *status predicted F:125,245/Blnding site: carbohydrate (Asn) (covalent) *status predicted	
55.8%; Score 914; DB 1; I	Db 186 GELKWGTDEAQFIYILGRRSKQHLRMVFDEYLKISGKPIERSIRAELSGDFEKLKLAVVK 245
Similarity 58.0%; Pred. No. 1.2e-51; 2; Conservative 51; Mismatches 81;	250 SIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRRNFATSLYSMIKG
QY 14 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL 73	240
Db 6 GTVKAASGFNAAEDAQTLRKAMKGLGTDEDAILNVLAYRSTAQRQEIRTAYKTTIGRDLM 65	Qy 310 DTSGDYKKALL-LLSGEDD 327

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Note: the list of introns is incomplete
C; Superfamily: annexin vII; annexin repeat homology
C; Superfamily: annexin vII; annexin repeat homology
C; Superfamily: annexin viet annexin repeat homology (AXI)
F; 203-274/Domain: annexin repeat homology (AXI)
F; 214-230/Region: endonexin fold #status predicted
F; 275-346/Domain: annexin repeat homology (AXI)
F; 286-302/Region: endonexin fold #status predicted
F; 388-430/Domain: annexin repeat homology (AXI)
F; 370-386/Region: endonexin fold #status predicted
F; 345-461/Region: endonexin fold #status predicted
F; 445-461/Region: endonexin fold #status predicted
F; 61,113/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1.505 <7000.
A; Cross-references: EMBL: 211742; NID: 977; PIDN: CAA77801.1; PID: 978
A; Towle, C.A.; Weissbach, L.; Treadwell, B.V.
Blochim. Blophys. Acta 1131, 223-225, 1992
A; Title: A. Atternatively spliced annexin XI transcripts encode proteins that differ nea
A; Reference number: S36136; MUID: 92305067; PMID: 1535225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:211742
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
                                                                                        C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 10-Reb-1995 #text_change 22-Jun-1999
C;Accession: S23447; S36136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Best Local Similarity 54.9%; Pred. No. 2.9e-48;
Matches 173; Conservative 58; Mismatches 84;
                                                                                                                                                                   A;Reference number: $23447
A;Accession: $23447
A;Moleonion:
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GDYRKILLKICGGND
                                                                             annexin XI form B - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-77 <TO2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       annexin XI - rabbit
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A;Molecule type: potein
A;Residues: 213.223, X',225-226,319-325,'G',327-328,'X',330-333,'Q',335-339;441-450,'X',
A;Experimental source: lung
A;Experimental source: lung
C;Comment: sequence modified after extraction from NCBI backbone
C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholig derstood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein; phospholipid bin
                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: GB.M82802; NID:g162673; PIDN:AAA30379.1; PID:g162674
A;Note: the authors did not translate the codon GAC for residue 503
A;Natutani, A: Usuda, N: Tokumitsuv, H:; Minami, H:; Yasui, K.; Kobayashi, R.; Hidaka, J. Biol. Chem. 267, 13498-13504, 1992
A;Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblast A;Reference number: A42909; MUID:92317074; PMID:1618851
                                                                                                                                                                           C; Species: Bos primigenius taurus (cattle)
C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C; Caccession: A42113; A42909; B42909; C42909; D42909
R; Towle, C.A.; Treadwell, B.V.
J. Biol. Chem. 267, 5416-5423, 1992
A; Title: Identification of a novel mammalian annexin. cDNA cloning, sequence analysis, A; Reference number: A42113; MUID:92184796; PMID:1372001
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A.Note: the list of introns is incomplete
C.Superfamily: annexin vII; annexin repeat homology
C.Superfamily: annexin repeat homology
C.Superfamily: annexin repeat homology AXI>
F.201-272/Domain: annexin repeat homology AXI>
F.212-228/Region: endonexin fold #status predicted
F.213-344/Domain: annexin repeat homology AXI>
F.344/Domain: annexin repeat homology AXI>
F.366-384/Region: endonexin fold #status predicted
F.356-38/Domain: annexin repeat homology AXI>
F.343-503/Domain: annexin repeat homology AXI>
F.343-503/Domain: annexin fold #status predicted
F.343-459/Region: endonexin fold #status predicted
F.351/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                        N; Alternate names: calcyclin-associated protein peptide, CAP-50
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Pred. No. 2.9e-48;
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  DTSGEYKKALLKLCEGDDD 324
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GDYRKILLKICGGND 503
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Best Local Similarity 54.99
Matches 173; Conservative
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A, Residues: 1-503 <TOW>
306
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Across references: GB:L19605; NID:g457128; PIDN:AA19734.1; PID:g457129
C;Genetics:
A;Gene GB:ANX11
A;Cross references: GB:313076
A;Gene GB:ANX1
A;Cross references: GB:313076
A;Map position: 9g11-9g22
C;Superfamily: annexin VII; annexin repeat homology
C;Superfamily: annexin repeat homology AXX1
F;203-274/Domain: annexin repeat homology AXX2
F;258-430/Domain: annexin repeat homology AXX2
F;358-430/Domain: annexin repeat homology AXX3
F;358-430/Domain: annexin repeat homology AXX4
F;358-430/Domain: annexin repeat homology AXX4
F;358-430/Domain: annexin repeat homology AXX4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
                                                                                                                                                                                                                                                                                                                                                                                                                                       52.2%; Score 855; DB 2; 53.3%; Pred. No. 1.3e-47; tive 61; Mismatches 86
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Best Local Similarity
Matches 168; Conserv
                                           A; Molecule type: mRNA
A: Residues: 1-505 <MIS>
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A; Molecule type: protein

A; Residues: 104-141;213-223, 'X', 225-231;254-263;271-280;285-291, 'X', 293-300, 'X', 302-309;

C; Comment: This protein binds specifically to calcyclin in a Ca2+ dependent manner.

C; Superfamily: annexin VII; annexin repeat homology C; Reywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin

F; 201-272/Comain: annexin repeat homology cannow an annexin repeat homology cannow an annexin repeat homology cannow an annexin fold #status predicted
                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein

R; Residues: 104-141;213-231,254-262;270-280;285-309;319-337;429-448;478-492 <TK2>
R; Residues: 104-141;213-231,254-262;270-280;285-309;319-337;429-448;478-492 <TK2>
R; Tokumitsu, H.; Mizuteni, A.; Minami, H.; Kobayashi, R.; Hidaka, H.
J. Biol. Chem. 267, 8919-8924, 1992
J. Filol. Chem. 267, 8919-8924, 1992
A; Title: A calcyclin-associated protein is a newly identified member of the Ca(2+)/phoss A; Reference number: A38250; MUID:92250478; PMID:1533622
A; Accession: A38250
           C;Accession: JH0694; PH0950; A38550; Ps0263
R;Tokumitsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H.
Biochem. Biophys. Res. Commun. 186, 1277-1235, 1992
A;Title: Molecular cloning of rabbit CAP-50, a calcyclin-associated annexin protein.
A;Reference number: JH0694; MUID:92378579; PMID:1380798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
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C;Date: 07-Jul_1995 *sequence_revision 07-Jul-1995 *text_change 13-Aug-1999
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                         A; Cross-references: DDBJ:D10883; NID:9471147; PIDN:BAA01705.1; PID:9471148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: A53152
R;Misaki, Y.; Pruijn, G.J.M.; van der Kemp, A.W.C.M.; van Venrooij,
J. Biol. Chem. 269, 4240-4246, 1994
A;Title: The 56K autoantigen is identical to human annexin XI.
A;Reference number: A53152; MUID:94140847; PMID:7508441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 52.7%; Score 863; DB 1;
Best Local Similarity 54.3%; Pred. No. 3.9e-48;
Matches 171; Conservative 60; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;273-344/Domain: annexin repeat homology <AXZ>
F;284-300/Region: endonexin fold #status predicted
F;356-428/Domain: annexin repeat homology <AX3>
F;365-384/Region: endonexin fold #status predicted
F;432-503/Domain: annexin repeat homology <AX4>
F;432-503/Domain: endonexin fold #status predicted
F;443-459/Region: endonexin fold #status predicted
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A; Residues: 1-503 <TOK>
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OM protein . protein search, using sw model

August 22, 2003, 21:28:42; Search time 8.66667 Seconds (without alignments) 1774.354 Million cell updates/sec Run on:

US-09-970-969-4 1639 1 MAGCGHMAQVLRGTVTDFPKGDTSGDYKKALLLLSGEDD 327 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

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Iwasaki A., Suda M., Nakao H., Nagoya T., Saino Y.,
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AAB40047.1;

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(Anchorin CII).
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                 Acetylation.
INIT_MET
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P48036;
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                                    REPEAT
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MOD_RES
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                                                                                                                            Match
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                                                                                  GROLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
                                                                                            KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK 308
                                                                                                                                                                                                               68
                                                               9
                                                       LRAIKOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFO
                                                                                                                                                               AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                                                                                                                                                                          9 AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-10 (Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Green B.N., Aitken A.;
"Novel isoforms of CaBP 33/37 (annexin V) from mammalian brain:
structural and phosphorylation differences that suggest distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B., Patel Y.,
                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Donato R.,
         Length 319;
                          1; Indels
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Learmonth M.P., Howell S.A., Harris A.C.M., Amess
Glambanco I., Blanchi R., Pula G., Ceccarelli P.,
       Score 1585; DB 1;
Pred. No. 3.2e-95;
); Mismatches 1
                                                                                                                                                                                                                                                                                                              320 AA
                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                      GDTSGDYKKALLLCGEDD 319
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SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
       96.78;
                         Matches 318; Conservative
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
                 Similarity
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P81287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GRDLLDDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK
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01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
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Sciurognathi; Muridae; Murinae; Mus
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .P.
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ξ
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MEDLINE-96422179; PubMed-8824796;
MEDLINE-96422179; PubMed-8824796;
MEDLINE-Garcia M.I., Kozzak C.A., Morgan R.O., Fernandez
"Mouse annexin V chromosomal localization, cDNA sequence
conservation, and molecular evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length
                                                                                                                                                                                                                                                                                      ACETYLATION (BY SIMILARITY):
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1536.5; DB 1; Length
Pred. No. 4.2e-92;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                        50FCE18E95F19CB0 CRC64;
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
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SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.7%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 31:151-157(1996).
                                                                                                                                                                                                                                                                                                                                                                                            35942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 96.6
Matches 309; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            320 AA;
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RAT
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                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as iong as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                 calcium and phospholipid.
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RGTVTDFPGFDERADAETLRKAMKGLGTDEES1LTLLTSRSNAQRQE1SAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGTVTDFPGFDGRADAEVLRKAMKGLGTDEDS1LNLLTSRSNAQROE1AQEFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                               ACTS AS
                                                                                                           for
                                        retrovirus.";
J. Blochem. 337:125-131(1999).

-I- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS !

-I NUDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX,
WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.

-I- SUBUNIT: MONOMER. BINDS ATRX (By similarity).

-I- DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
     Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.R., Bances P., Fernandez M.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 319;
                               "Mouse annexin V genomic organization includes an endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 4.
55055BAF2ELC36B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.9e-88;
9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.3%; Score 1479.5; 93.7%; Pred. No. 1.96
                                                                                                                                                                                                                                                                  AJ230108; CAA13092.1; AJ230110; CAA13092.1; JOINED. AJ230111; CAA13092.1; JOINED. AJ230114; CAA13092.1; JOINED. AJ230116; CAA13092.1; JOINED. AJ230119; CAA13092.1; JOINED. AJ230120; CAA13092.1; JOINED. AJ230121; CAA13092.1; JOINED. AJ230122; CAA13092.1; JOINED. AJ230123; CAA13092.1; JOINED. AJ230123; CAA13092.1; JOINED. AJ230123; CAA13092.1; JOINED. AJ230124; CAA13092.1; JOINED.
MEDLINE-99072820; PubMed-9854034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35752 MW;
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InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
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Best Local Similarity 93.77
Matches 296; Conservative
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238
313
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94
178
278
253
319 AA;
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SWISS-2DPAGE; P4803
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SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                        01-57871990 (Rel. 14, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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istructure of rat annexin V gene and molecular diversity of 1ts
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MEDLINE-93369587; PubMed-8362244;
Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
"Rat annexin V crystal structure: Ca(2+)-induced conformational
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Pepinsky R.B., Tizard R., Mattallano R.J., Sinclair L.K.,
Miller G.T., Browning J.L., Chow B.P., Burne C., Huang K.S.,
Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.;
Frive distinct calcium and phospholipid binding proteins share
homology with lipocortin I.*;
J. Biol. Chem. 263:10799-10811(1988).
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Blochemistry 37:8004-8010(1998).
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Science 261:1321-1324(1993).
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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
SMART; SM00335; ANX; 4.

PROSITE; PS00223; ANNEXIN; 4.

Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
Placenta; Acetylation; 3D-structure.

INTT_MET 20 80 ANNEXIN 1.
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Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
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1A8A; 17-JUN-98.
1A8B; 17-JUN-98.
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                                                                                                                                                         01-FEB-1996 (Rel. 33, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
(Anchorin CII).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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MEDIINE=88186917; PubMed=283352;
Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
Deutzmann R., Mollenhauer J., von der Mark R.;
"The structure of anchorin CII, a collagen binding protein isolated from chondrocyte membrane.";
                                                   88.8%; Score 1455.5; DB 1; Length 318; 91.8%; Pred. No. 6.7e-87; ive 12; Mismatches 13; Indels 1;
35613 MW; 1A755A7C11FA11CE CRC64;
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Moss S.E., Crumpton M.J.;
"Alternative splicing or cloning artefact?";
Trends Biochem. Sci. 14:325-325(1989).
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REVISIONS.
MEDILINE-9043721; PubMed-2159478;
MEDILINE-9043721; PubMed-2159478;
Ernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
Deutzmann R., Mollenhauer J., von der Mark K.;
"The structure of anchorin CII, a collagen binding protein isolated from chondrocyte membrane":
J. Biol. Chem. 265:8344-8344(1990).
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STRAIN-White leghorn; TISSUE-Liver;
MEDLINE-94215900; PubMed-8163186;
Fernandez M.P., Fernandez M.R., Morgan R.O.;
"Structure of the gene encoding anchorin CII (chick annexin V).";
Gene 141:179-186(1994).
                                                                                                                                                                                                                                                                                TISSUE-Liver;
MEDLINE-93249384; PubMed-8484740;
Boustead C.M., Brown R., Walker J.H.;
"Isolation, characterization and localization of annexin V from
                                                                                     Pfaeffle M., Rugglero F., Hofmann H., Fernandez M.P., Selmin
Yamada Y., Garrone R., von der Mark K.;
EMBO J. 9:1336-1336(1990).
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Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
SMART; SM00335; ANX; 4.
PR057TF; PS00223; ANNEXIN; 4.
ANNEXIN; Calcium/Phospholipid-binding; Repeat; 3D-structure.
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EMBL: U01671; AAB39917.
EMBL: U01672; AAB39917.
EMBL: U01673; AAB39917.
EMBL: U01675; AAB39917.
EMBL: U01676; AAB39917.
EMBL: U01677; AAB39917.
EMBL: U01677; AAB39917.
EMBL: U01677; AAB39917.
PIR: A35381; LUCH5.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae, Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto T., Hikono T., Abe S.I.; ** **Ifferential expression of annexin V during spermatogenesis in the
                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                               Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                 36198 MW; 43E2983F86797025 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            78.0%; Score 1279; DB 1; 78.1%; Pred. No. 1.5e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SPP-2003 (Rel. 42, Last annotation update)
Innexin AS (Annexin V).
                                                                                                                                                                                                                                                                                                                                                                                                                           38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 QKDTSGDYRKALLLLCGGDD 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308 KGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   newt Cynops pyrrhogaster.";
Dev. Genes Evol. 206:64-71(1996).
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 78.1%
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
TISSUE-Test1s;
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANXS_CYNPY
P70075;
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[1]
SEQUENCE FROM N.A.
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  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252
                                                                                                                                                                                                                                                                                                                                                                                               73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
                                                                                                                                                                                                                                                                                                                                                                                                           KOVY EEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIPAYLAETLYYAMKGAGTODHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307
                                                                                                                                                                                                                                                                                                                                                        72
                                                                                                                                                                                                                                                                                                                                                                   13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
          MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY). DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
 FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                 Length 323;
                                                                                                                                                                                                                                                                                                             Query Match 66.3%; Score 1086; DB 1; Length 3
Best Local Similarity 67.9%; Pred. No. 4e-63;
Matches 214; Conservative 45; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                            044B31AC28164CE2 CRC64;
                                                                                                                                                                                                                                          Repeat.
                                        BELONGS TO THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            672 AA.
                                       SIMILARITY: BELONGS TO THE ANNEXIN FAMII
SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                            ANNEXIN 2.
ANNEXIN 3.
                                                                                                                                                                                                                 SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                ANNEXIN 4
                                                                                                                                                                                                                                                   ANNEXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                          98 158 AN
182 242 AN
257 317 AN
323 AA; 35981 MW;
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                                                                                                                                                                          InterPro; IPR001464; Annexin.
                              calcium and phospholipid.
                                                                                                                                                     EMBL; D64134; BAA11012.1; -. HSSP; P08758; 1AVH.
                                                                                                                                                                                  Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 GDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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P08133;
                                                                                                                                                                                                                  SMART; SM
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                         133
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                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                REPEAT
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Attausherg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Mans S.I., Wang J., Hsteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Schouchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Roberzation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                      Suedhof T.C., Slaughter C.A., Leznicki I., Barjon P., Reynolds G.A.; "Human 67-kDa calelectrin contains a duplication of four repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
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-i- PTM: PHOSPHORYLATED IN RESPONSE TO GROWTH FACTOR STIMULATION.
-i- MISCELLANBOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
-i- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-i- SIMILARITY: Contains 8 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. MOI. BIOI. 260:638-643(1996).
-i- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF CA(2+) FROM INTRACELLULAR STORES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-89380132; PubMed-2528541; Iwasaki A., Suda M., Watanabe M., Nakao H., Hattori Y., Nagoya T., Saino Y., Shidara Y., Maki M.; Saino Y., Shidara Y., Maki M.; Structure and expression of CDNA for calphobindin II, a human placental coaqulation inhibitor."; J. Biochem. 106:43-49(1989).
                                                                                                         "Primary structure of the human, membrane-associated Ca2+-binding protein p68 a novel member of a protein family."; EMBO J. 7:21-27(1988).
                               Crompton M.R., Owens R.J., Totty N.F., Moss S.E., Waterfleld M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96326697; PubMed-8709144;
Benz J., Bergner A., Hofmann A., Demange P., Goettig P., Liemann
Huber R., Voges D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshizaki H., Mizoguchi T., Arai K., Shiratsuchi M., Shidara Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure and properties of calphobindin II, an anticoagulant protein from human placenta."; J. Biochem. 107:43-50(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found in 35-kDa lipocortins.";
Proc. Natl. Acad. Sci. U.S.A. 85:664-668(1988).
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-88124902; PubMed-2963335;
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MEDLINE-22388257; PubMed-12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90236978; PubMed-2139657;
MEDLINE-88196081; PubMed-3258820;
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                                                                                                                                                  InterPolicy in Producted and Annexin.

Pfam: Profolg; annexin: 8.

Profolg; annexin: 8.

Profolg; annexin: 8.

SMART: SW00335; ANX: 8.

SMART: SW00335; ANX: 8.

Annexin: Calcium/phospholipid-binding; Repeat; Acetylation; Phosphorylation; 3D-structure.

Prosphorylation; 3D-structure.

REPEAT 28 88 ANNEXIN 1.

REPEAT 28 88 ANNEXIN 1.

REPEAT 100 160 ANNEXIN 2.
                                                                                                                                                                                                                                                                                                                                                                      ; Score 932; DB 1; Length 672; ; Pred. No. 7.8e-53; 52; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                               ACETYLATION.
IE -> MK (IN REF. 2).
S -> T (IN REF. 2).
E -> D (IN REF. 1).
H; 2829237029BDIDCB CRC64;
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                                                                                                                                                                                                                                       ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 5.
ANNEXIN 6.
ANNEXIN 6.
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p14824;
01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                     75742 MW;
                                                                                   EMBL; Y00097; CAM68286.1; --
EMBL; J03578; AAA35656.1; --
EMBL; BC017046; AAH17046.1; --
PTR; JU0032; AQHUG8.
PDB; 1M91; 07-AUG-02.
                                                                            EMBL; D00510; BAA00400.1; -.
                                                                                                                                                                                                                                                                                                                                                                       56.9%;
58.1%;
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310 GEYKKTLLKLSGGDD 324
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                                                                                                                                  Genew; HGNC:544; ANXA6.
MIM; 114070; -.
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554
618
672 AA;
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MOD_RES
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 IEDLKYELTGKFERLIVNLMRPLAYCDAKEIKDAISGIGTDEKCLIEILASRTNEOMHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF CA(2+) FROM INTRACELLULAR STORES.
-1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-1- MISCELLANBOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
-1- SIMILARITY: CONTAINS 8 annexin repeats.
                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
01-APR-1990 (Rel. 14, Last sequence update)
1-SEP-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocottin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)
                                                                                                                                                                                                                                                                                                                                       Moss S.E., Crompton M.R., Crumpton M.J.; "Molecular cloning of murine p68, a Ca2+-binding protein of the lipocortin family.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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MGD; MGI:88255; Anxa6.
InterPro; PR001464; Annexin.
Pfam; PF00191; annexin; 8.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
SMART; SM00335; ANX; 8.
PROSTITE; PS00223; ANX; 8.
Annexin; Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.9%; Score 932; DB 1; 59.0%; Pred. No. 7.8e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Mismatches
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 5.
ANNEXIN 6.
ANNEXIN 6.
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                                                                                                                                                                                                                                                                                                               MEDLINE-89030687; PubMed-2972541;
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Matches 186; Conservative
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532
607
672 AA;
                                                                                                                                                                                                       NCBI_TaxID-10090;
                                                                                                       ANXA6 OR ANX6.
                                                                                                                                                                                                                                                            SEQUENCE FROM STRAIN-BALB/C
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SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE-22388257; PubMed-12477932;

MEDLINE-22388257; May S. L., Shenmen C. M., Schuler G.D.,

MEDLINE-22388257; May S. L., Wang J., Maleh F.,

MEDLINE-22388257; May S. L., Wang J., Maleh F.,

MEDLINE-22388257; MAY PERCENT G.J., Abramson R.D., Mullahy S.J.,

MEDLINE-2238825; MOTHON M., Sodergren R.J., Malek J.A., Gunarane P.H.,

RICHARGS S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

RICHARGS S.A., MCEwan P.J., McKernan R.J., Malek J.A., Gunarane P.H.,

MILIAGON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

MILIAGON D.K., Muzny D.M., Garcia A.M., Gabs R.A.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Milling M., Madan A., Schautz J., Myers R.M.,

Butterfield Y.S.N., Kzzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and Initial analysis of more than 15,000 full-length
                                      190 KWGTDEAQFIYILGNRSKQHLRLVFDEYLKTTGKPIEASIRGELSGDFEKLMLAVVKCIR 249
                                                                                                                                                                                                                                                                                                  P09525; Q96F33; Q9BWKI; O1-MAR-1989 (Rel. 10, Created) O1-OCT-1996 (Rel. 34, Last sequence update) 15-SEP-2003 (Rel. 42, Last sequence update) Annexin A4. (Annexin IV) (Lippocortin IV) (Endonexin IV) (Chromobindin 4) (Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II) (PP4-X) (35-beta calcimedin) (Carbohydrate-binding protein P33/P41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of human p33/41 (annexin IV), a Ca2+ dependent carbohydrate-binding protein with monoclonal anti-annexin IV antibodies, AS11 and AS17."; Biol. Pharm. Bull. 20:224-229(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88309022; PubMed-2970257;
Grundmann U., Amann E., Abel K.-J., Kuepper H.A.;
"Isolation and expression of CDNA coding for a new member of the
phospholipase A2 inhibitor family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92155721; PubMed-1346776;
Talt J.F., Smith C., Frankenberry D.A., Miao C.H., Adler D.A.,
Disteche C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Chromosomal mapping of the human annexin IV (ANX4) gene."; Genomics 12:313-318(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Behring Inst. Mitt. 82:59-67(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-97239215; PubMed-9084877;
                                                                                                                             313 GDYKKALLLLSGEDD 327
                                                                                                                                                       |:||||| | | ||
310 GEYKKALLKLCGGDD 324
                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANXA4 OR ANX4.
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                                                                                                                                                                                                                                         RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/of send an email to license@isb-sib.ch).
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                                                                                                                                     phospholipase A2 inhibitors from human placenta. Evidence against a mechanistically relevant association between enzyme and inhibitor."; J. Biol. Chem. 263:18657-18663(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY. -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY. -!- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7. Mol. Biol. 216:219-221(1990).
-!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRARDE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                       Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W., de Haen C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91073383; PubMed-2254922; Freemont P.S., Driessen H.P.C., Verbi W., Crumpton M.J.; Crystallization and preliminary X-ray crystallographic studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                             'Sedimentation equilibrium analysis of five lipocortin-related
                                                                                                                                                                                                                                                                                                             Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi T., Hendrickson L.E., Fujikawa K.; Placental anticocalunt proteins: isolation and comparative characterization four members of the lipocortin family.";
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16B19E01500350F7 CRC64;
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; Pred. No. 1.2e-52;
53; Mismatches 78;
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PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                         SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
MEDLINE-89118212; PubMed-2975506;
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ANNEXIN 2.
ANNEXIN 3.
SEQUENCE OF 26-55; 98-123 AND 279-307.
MEDLINE-89066652; Pubmed-2974032;
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EMBL; M82809; AAA51740.1; -.
EMBL; D78152; BAA11227.1; ALT_INIT.
EMBL; BC00182; AAH00182.1; ALT_INIT.
EMBL; BC011659; AAH11659.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 27:6268-6276(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
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35751 MW;
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58.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human placental annexin IV."
J. Mol. Biol, 216:219-221(19
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SWISS-2DPAGE; P09525; HUMAN.
PMMA-2DPAGE; P09525; -.
Genew; HGNC:542; ANXA4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY
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CONFLICT
SEQUENCE
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PIR; A27107; LUPG4
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       DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK·133
                   184
                                                                                                                                        313
                                                                                                                                                   ANX4_PIG STANDARD; PRT; 318 AA.
P08132; Q29306;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
(Protein II) (P32.5) (Placental anticoagulant protein I) (PAP-II)
ANX44 OR ANX4.
                                                              QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
                                                                                           WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                    254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Intestinal epithelium;
MEDILNE-87275850; Pubmed-2956093;
WHEDER K., Johnsson N., Plessmann U., Van P.N., Soling H.-D., Ampe C., Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The amino acid sequence of protein II and its phosphorylation site for protein kinase C; the domain structure Ca2+-modulated lipid binding proteins."; EMBO J. 6:1599-1604(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcium and phospholipid.
MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
SIMILARITY: CONTAINS 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; F14682; CAA23194.1; -.
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|DYRKVLLVLCGGDD 318
                                                                                                                                                                                DYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                         scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 DDLKSELSGNFEQVILGMWTPTVLYDVQELRRAMKGAGTDEGCLIEILASRTPEEIRRIN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 QVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eur. J. Biochem. 230:741-751(1995).
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MEDLINE=2531313; PubMed=7607247;
Tan H., Josic D., Lim Y.P., Reutter W.;
"CDNA cloning and tissue-specific regulation of expression of rat calcium-binding protein 65/67. Identification as a homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
45-SEP-2003 (Rel. 42, Last annotation update)
66-FEB-1996 (Rel. 42, Last annotation update)
67-FEB-1996 (Rel. 42, Last annotation update)
67-FEB-1996 (Rel. 42, Last annotation update)
67-FEB-11)
67-FEB-1996 (Rel. 33, Created III)
67-FEB-11)
67-FEB-12)
67-FEB-13, Created IIII)
67-FEB-11)
67-FEB-13, Created IIII)
67-FEB-11)
67-FEB-13, Created IIII)
67-FEB-13, Created IIIII)
67-FEB-13, Created IIIII
67-FEB-13, Created IIIII
67-FEB-13, Created IIIII
67-FEB-13, Created IIII
67-FEB-13, Create
                                                                                                        PRINTS; PR00196; ANNEXIN.
Prodom; PD0001943; Annexin; 4.
PROSITE; PS00223; ANNEXIN; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calclum/phospholipid-binding; Repeat; Phosphorylation;
INIT_MET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%; Score 921; DB 1; Length 31
58.6%; Pred. No. 1.6e-52;
ive 51: Mismatches 79; Indelb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACETYLATION (PROBABLE).
PHOSPHORYLATION (BY PKC).
FA7D9CE2B7C631E8 CRC64;
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Best Local Similarity 58.6%; Pred. No. 1.be-
Matches 184; Conservative 51; Mismatches
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ANNEXIN 2.
ANNEXIN 3.
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318 AA; 35697 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                 InterPro; IPR001464; Ani
Pfam; PF00191; annexin;
                                                                                                                                                                                                                                                                                                                                                      92
154
238
313
P13214; IANN
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NCBI_TaxID=10090;
                                                                    STRAIN-C3H/HeJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 180;
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                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                           252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                       13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                  133 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 KWGIDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                             MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
SIMILARITY: Contains 8 annexin repeats.
CA(2+) FROM INTRACELLULAR STORES.

DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                    Length 672;
                                                                                                                                                                                                                                                                                                                                                 56.2%; Score 921; DB 1; Length 67
58.7%; Pred. No. 4e-52;
tive 40; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                      ANNEXIN 8.
BBEE798A9CAB1511 CRC64;
                                                                                                                                                                      Property: IPRO01464; Annexin.
Pfam; PF00191; annexin; 8.
PRINTS; PR00196; ANNEXIN.
PRODON: PD000143; Annexin; 8.
SMART; SM00335; ANX; 8.
PROSITE; PS00223; ANNEXIN; 7.
Annexin; Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 5.
ANNEXIN 6.
                                                                                                                                                                                                                                                                                                                       667 . A
75622 MW;
                                                                                                                                            EMBL; X86086; CAA60040.1; -. PIR; S65683; S52844.
HSSP; P79134; 1AVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|||||| | | || GEYRKALLKLCGGDD 324
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 58.7% Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Annexin A4 (Annexin IV).
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                                                                                                                                                                                                                                                                                                   532
532
607
672 AA;
                                                                                                                                                                                                                                                                                                                                                            Similarity
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P97429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194 WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL
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                                                                                                                                                                                                 Sable C.L., Shannon J., Riches D.W.H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROFEIN WHICH PROMOTES.
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY (BY SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: Contains 4 annexin repeats.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 82 ANNEXIN 1.
94 154 ANNEXIN 2.
178 238 ANNEXIN 3.
253 313 ANNEXIN 4.
318 AA; 35858 MW; 53FAC7AD8006BC0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:88030; Anxa4.
MGD; IPR001464; Annexin.
Pfan; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
SMAPE; SM00315; ANNEXIN; 4.
PROSITE; PS00223; ANNEXIN; 4.
PROSITE; PS00223; ANNEXIN; 4.
INIT, MET

22

REPEAT

22

ANNEXIN I.
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.9%; Score 916; DB 1; 57.3%; Pred. No. 3.4e-52; ative 58; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U72941; AAB40697.1; -. HSSP; P13214; 1ANN.
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                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
(Protein II) (P32.5) (Placental anticoagulant protein II) (PAP-II)
(P93.41).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96205957; PubMed=8631806;
Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;
"Characterization of carbohydrate-binding protein p33/41: relation
with annexin IV, molecular basis of the doublet forms (p33 and p41),
and modulation of the carbohydrate binding activity by
phospholipids.";
j. Blol. Chem. 271:7679-7685(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
WEDLINE=98070213; PubMed=9405281;
Zanotti G., Malpeli G., Gliubich F., Folli C., Stoppini M., Olivi L.,
Savota A., Berni R.;
"Structure of the trigonal crystal form of bovine annexin IV.";
"Structure of the trigonal crystal form of bovine annexin IV.";
"Structure of the trigonal crystal form of bovine annexin IV.";
-1- SUBUNIT: Monomer.
-1- SUBUNIT: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-1- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-89050088; PubMed-2847715; Hamman H.C., Gaffey L.C., Lynch K.R., Creutz C.E.; "Cloning and characterization of a cDNA encoding bovine endonexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lochem. Biophys. Res. Commun. 156:660-667(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sutton R.B., Sprang S.R.;
Submitted (SEP-1995) to the PDB data bank
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EMBL; X13627; CAA31954.1; --
EMBL; D78178; BAA11243.1; --
PIR; AA1578; LUBO4.
PDB; IANN; 29-JAN-96.
PDB; IANN; 25-APR-01.
InterPro; IPR001464; Annexin.
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ProDom; PD000143; Annexin; 4.
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                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromobindin 4).";
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                                                                                                                                                                                                                                                                                                                                                                                            *CBI_TaxID=9913;
                                                                                                                                                                                                                                                                  ANXA4 OR ANX4.
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                                         ANX4_BOVIN
P13214;
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DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
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P5094;
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule membrane associated protein) (ZAP36).
ANX44 OR ANX4.
Canis familiaris (Dog).
Calcium/phospholipid-binding; Repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.8%; Score 914; DB 1; Length 31 Best Local Similarity 58.0%; Pred. No. 4.5e-52; Matches 182; Conservative 51; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35757 MW; 86BDBDF349D774FD CRC64;
                                                                                                        REF.
                                                                                           REF.
                           ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
L -> V (IN R
E -> K (IN R
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            INIT_MET
REPEAT
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CONFLICT
CONFLICT
HELIX
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 Annexin;
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ANX4_CANFA
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73 64

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Similarity
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=9031;
                                                             ANXA6 OR ANX6.
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                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 KSAYFAERLYKSMKGLGTDDNTLIRVMVSRAEIDMMDIRESFKRLYGKSLYSFIKGDTSG
                                                                               FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY). DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                              calcium and phospholipid.
MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
Chordata; Craniata; Vertebrata; Euteleostomi;
Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                               81; Indels
                                                                     Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                      42EF5B89179B4863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 901; DB 1;
; Pred. No. 3.1e-51;
54; Mismatches 81;
                                                                                                                                            SIMILARITY: BELONGS TO THE ANNEXIN FAMILY. SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      671 AA.
                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                          55.0%; Score 901;
                                                                                                                                                                                                                                                                                                                                                                       ANNEXIN 2.
ANNEXIN 3.
                                                                                                                                                                                                                                                                                                                                            Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                               ANNEXIN 1
                                                                                                                                                                                                                                                                                                                                                                                              ANNEXIN
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                                       SEQUENCE FROM N.A.
STRAIN-Mongrel; TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                       35681 MW;
                                                                                                                                                                                                                                                                            Interpro: IPR001464; Annexin.
Pfam; PP00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
Procom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                                                                                                                                          EMBL; D38223; BAA07398.1; -. HSSP: P13214; LANN.
                                                                                                                                                                                                                                                                                                                               PROSITE; PS00223; ANNEXIN; 4.
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                                                                                                                                                                                                                                                                                                                                                            22 8
94 15
178 23
253 3
 Sukaryota; Metazoa;
           Eutheria;
                                                                                                                                  (BY SIMILARITY)
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                   NCBI_TaxID-9615;
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REPEAT
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SOCOCOCORANGERACION
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                                                                                                                                                                                                                                                                                                                                                                                         Cao X., Genge B.R., Wu L.N., Buzzi W.R., Showman R.M., Wuthier R.E.; "Characterization. oloning and expression of the 67-kDA annexin from chicken growth plate cartilage matrix vesicles."; Biochem. Biophys. Res. Commun. 197:556-561(1993).
--- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULART THE RELEASE OF CA(2+) FROM INTRACELLOLAR STORES (BY SIMILARITY).
--- DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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; Pred. No. 1.5e-50;
51; Mismatches 83;
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PROSITE; PS00223; ANNEXIN; 5.
Annexin; Calcium/phospholipid-binding; Repeat.
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ANNEXIN 5.
ANNEXIN 6.
ANNEXIN 7.
ANNEXIN 7.
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HSSP, P79134; 1AVC.
InterPro; IPR001464; Annexin.
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57.7%;
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
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Matches 184; Conservative
                                                                                                                                                                  Gallus gallus (Chicken).
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258
370
442
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671 AA;
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ογ	250 SIRSIPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKG 309	
qq	246 CVRSTAEYFAERLYKAMKGLGTRDNTLIHIMVSRSEIDMLDIREVFRTKYDKSLHNMIKE 305	
Qy	310 DYSGDYKKALL-LLSGEDD 327	
qq	306 DISGEYKKALLKLCEGDDD 324	

²⁴⁶ CVRSTAEYFAERLYKAMKGLGTRDNTLIHIMVSRSEIDMLDIREVFRTKYDKSLHNMIKE 305

Search completed: August 22, 2003, 21:33:38 Job time: 9.66667 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:
August 22, 2003, 21:29:22; Search time 31.6667 Seconds

(without alignments)
2664.733 Million cell updates/sec

Title:
US-09-970-969-4
Perfect score:
1639
Sequence:
1 MAGGGGHMAQVLRGTVTDFP......RGDTSGDYKKALLLLSGEDD 327
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched:
830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters:
830525
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 08
Maximum Maxch 1008
Listing first 45 summaries
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Database : SPTREMBL_23:*

1: Sp_archea:*
2: sp_bacteria:*
3: sp_lung1:*
4: sp_human:*
5: sp_inwertebrate:*
6: sp_inwertebrate:*
7: sp_mhc:*!
8: sp_ombc:*!
10: sp_ombc:**
11: sp_rodent:*
11: sp_rodent:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_archius:*
16: sp_bacteriap:*
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16: sp_bacteriap:*
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16: sp_bacteriap:*
17: sp_archiap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q8wv69 homo sapien	Q99lal mus musculu	070371 rattus norv	093445 orygias lat	Q8cex0 mus musculu	Q991x6 mus musculu	Q8bss4 .mus musculu	093444 oryzias lat	093447 oryzias lat	090x16 xenopus lae	Q921fl mus musculu	Q8k2n9 mus musculu	095154 bos taurus	097529 oryctolagus	. OBclx9 mus musculu	0922a2 mis miscilli
OI.	Q8WV69	Q99LA1	070371	093445	QBCEXO	. 9xr660	Q8BSS4	093444	093447	Q90X16	Q921F1	Q8K2N9	Q95L54	097529	Q8C1X9	0922A2
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Query Match Length DB	320	319	302	317	476	299	673	320	208	321	503	327	327	327	323	463
Query Match	96.7	90.0	84.8	63.6	56.9	56.9	56.7	52.8	52.2	51.8	51.7	51.3	51.0	50.2	48.7	47.2
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Result No.	-	7	m	❖	S	9	7	60	6	10	11	12	13	34	15	16

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Qy Dp

QBvin2 rattus norv QBbp75 mus musculu QBn161 bombyx mori QB1918 drosophila Q921d0 mus musculu	Q9n159 bombyx mori Q9nq55 drosophlia Q8wpg9 bombyx mori Q8wph0 bombyx mori	Q27512 caenorhabdi Q9gng6 bombyx mori Q9n160 bombyx mori Q969d3 drosophila Q8tbv2 homo saolen	7 8 9	Q9vxg4 drosophila Q98sh7 brachydanio Q8hzm6 equus cabal Q92128 xenopus lae Q27864 caenorhabdi	QBccv9 mus musculu QBbcv9 mus musculu Q27473 caenorhabdi Q9xy89 schistosoma
11 Q8VIN2 11 Q8BP75 5 Q9NL61 5 Q8IGJ8 11 Q92ID0	5 Q9NL59 5 Q9NG55 5 Q8WPG9 5 Q8WPH0	5 Q27512 5 Q9GNG6 5 Q96NL60 5 Q969D3 4 OBTBV2	11 09CZI7 5 095v57 11 099JG3 6 08WJB5 5 09VXG3 13 093446	5 Q9VXG4 13 Q98SH7 6 Q8HZM6 13 Q92128 5 Q27864	11 Q8CCV9 11 Q8BSL2 5 Q27473 5 Q9XX89
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002 11	PRELIMINARY; PRT; 320 AA. (Tremblical, 20, Created) (Tremblical, 20, Last sequence update) (Tremblical, 23, Last annotation update)	Chordata Primates	Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY)!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS. InterPro: IPR001464; Annexin. Pfam: PF00191; annexin; 4. PRINTS: PR00196; ANNEXIN. PPINTS: PR00196; Annexin. 4.	X; 4. ANNEXIN; Calcium-h 35924 h 96.7%; 7ative
1 1 29 9 208WV69; 201-WAR-20 201-WAR-20 301-WAR-20 301-WAR-20 301-WAR-20 400000 sap 400000 sap 4000000000000000000000000000000000000	1 1 20 4069 PRELIMIN 20 40799; CTEMBLE 01-MAR-2002 (TTEMBLE 01-MAR-2003 (TTEMBLE	Human) azoa; erla; 6; N.A.	Strausberg R.; Submitted (DEC-2001) Submitted (DEC-2001)	.a: 0300
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LVNDMKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRA 122
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SWART; SM00335; ANX; ANX
PROSITE; PS00222; ANX
ANNEXIN; 3.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Ra
                                                                                                                                                                                                                                                                                                                                                TISSUE-Lung;

MEDLINE-99263163; PubMed-10129451;

MEDLINE-99263163; PubMed-10129451;

Men Y., Edelman J.L., Rang T., Sands G.;

Lipocortin V may function as a signaling protein for vascular endothelial growth factor receptor-2/Fik-1.";

Biochem Blophys. Res. Commun. 258:713-721(1999).

-I - DOMAIN: A PAIR OF ANNEXIN REPRATS MAY FORM ONE BINDING SITE CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

-I - SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

-I - SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

EMEL, AF051895; AAC06290.1; -.
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Last annotation update)
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Llarity 92.0%; Pred. No. 6.7e-90;
Conservative 12; Mismatches 12;
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                                                                                            GDYKKALLLL-SGEDD 327
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07,
23,
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                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat)
Eukaryota, Metazoa, Cho
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Best Local Similarity
Matches 276; Conserv
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Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

- I- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

CC -I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

-I- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

REMBL; BC003116; AAM0316.1; -...

RISSP; P14668; AAM8.

RISSP; P14668; AAM8.

RICEPPO; IPR001464; Annexin.

R InterPro; IPR001464; Annexin.

R Pfam; PR00191; annexin; 4.

R Prodom; P000143; Annexin; 4.

R SMART; SM00335; ANX; 4.
                           FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                               QAGELKWCTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEGLLLAV
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_raxID=10090;
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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Les 295; Conserv
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Annexin A5.
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                                                                                                                                                                                                                                                                                                                                                           124 IAAYRKEYDADLEEDICGDTSGHFKRLLVILLQANR--QTGVQEGDIENDAQVLFKAGEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                   Annexin max2.
Orgilas latipes (Medaka fish) (Japanese ricefish).
Bukaryota: Metazoa: Chordata; Cranidata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                         PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                  62; Indels
                                                                                                                                                                                                                                                                                                  AFD618681BAFF0FE CRC64;
                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                  63.6%; Score 1042; DB 13;
64.4%; Pred. No. 2.1e-65;
ive 48; Mismatches 62;
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Last sequence update)
                      317 AA
                                       Created)
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                      PRT;
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Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SWART; SW00335; ANX; 4.
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GDYRKALLLCGGDD 316
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                                              (TrEMBLrel. 08, (TrEMBLrel. 23,
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                                     01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                         al Similarity 64.4
203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                      PRELIMINARY;
                                                                                                                              SEQUENCE FROM N.A.
                                                                                                              NCBI_TaxID-8090;
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01-MAR-2003 (
01-MAR-2003 (
                                                                                                                                                                                                                                                                                                  SEQUENCE
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Matches
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133 KOVYEEEYGSSLEDDVVGDTSGYYQRMLVVILQANRDPDAGIDEAQVEQDAQALFQAGEL 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
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                                                                                                                                                                           The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KWGTDEEKFIT1FGTRSVSHLRKVFDKYMT1SGFQ1EET1DRETSGNLEQLLLAVVKSIR
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Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: A PAIR OR ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PROSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 8 ANNEXIN REPEATS.
EMBL; BC005595; AAN5595.1; -.
HSSP; P79134; 1AVC.
MGD; MGI:88255; Anxa6.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 8.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musimae; Mus
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                                                                                                                                                                                                                                                                                                                                                                  Length 476;
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                                                                                                                                                                                                                                                    60,770 IULL-1eng7...
Nature 420:563-573(2002).
EMBL; AK010342; BAC25291.1; -.
EMBL; AK010342; BAC25291.1; -.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             56.9%; Score 932; DB 11;
59.0%; Pred. No. 2e-57;
tive 48; Mismatches 81;
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                                                                                                                                  STRAIN-C57BL/6J;
MEDLINE-22354683; PubMed-12466851;
                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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311 GEYKKALLKLCGGDD 325
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                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 59.03
Matches 186; Conservative
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Mus musculus (Mouse).
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                                                                NCBI_TaxID=10090;
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312

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133 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                   KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                 SIPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                   RGTVTEASGFNPDDDAQKLREAMKGAGTDEAAIIKVLAHRTIAQRQRIKLAYKQSVGKDL
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                        131 VAAYKDAYERDLESDIIGDTSGHFQKMLVVLLQGTRENDDVVSEDLVQQDVQDLYEAGEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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                                                                                                                                                                                                                                                                                                                         Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99025617; PubMed-9809745; Osterloh D., Wittbrodt J., Gerke V.; "Characterization and developmentally regulated expression of four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                  update)
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DNA Cell Biol, 17:835-847(1998).

-!- DOMAIN: A PAAR OF ANNEXIN REPEATS MAY FORM ONE
CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

-!- SIMILARITY: COUPLING 4 ANNEXIN REPEATS.
                                                                                                                                                                                                                                                                                        Last sequence update)
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                                                                                                                                                                                                                                                                                                    Last annotation
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                                                                                                                                                                                                                                                 320
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08, Last sequ
23, Last anno
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ProDom; PD000143; Annexin; 4.
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                                                                                                                                                                                311 GEYKKALLKLCGGDD 325
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01-NOV-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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annotation
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                   PROSITE; PS00223; ANNEXIN; 8.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                     667;
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MEDLINE-2234683; Pubmed-12466851;
The FANTON CONSOITLUM,
the RIKEN GENOME Exploration Research Group Phase I & III
"Analysis of the mouse transcriptome based on functional 60,770 full-length CDNAs.";
Nature 420:563-573(2002);
EMBL; AK030728 BAC27101.1;
SEQUENCE 673 AA; 75885 MW; DCC5FC56CBD88809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81; Indels
                                                                                                                              80; Indels
                                                                                                     Length
                                                                          667 AA; 75260 MW; 363088A2A55CFF34 CRC64;
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Last annotation update)
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4.6e-57;
                                                                                                   ; Score 932; DB 11;
; Pred. No. 3.3e-57;
49; Mismatches 80;
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; Pred. No. 4.6e.
48; Mismatches
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            PD000143; Annexin; 8.
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GEYKKALLKLCGGDD 325
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Matches 186; Conservative
PRINTS; PR00196; ANNEXIN
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                         SM00335; ANX; 8
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                                                              Repeat.
SEQUENCE
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                                                                                                    Query Match
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Q8BSS4;
                         SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL 72
                                                                                                         ,
       SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                          annexins in the killifish medaka.";

DNA Cell Biol. 17:835-847(1998).

-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
                                                                                                                                                                              Annexin max4.
Oryzlas latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                                                                                             MEDLINE-99025617; PubMed-9809745;
Osterloh D., Wittbrodt J., Gerke V.;
"Characterization and developmentally regulated expression of four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                   Created)
                                                                                                                             PRT;
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InterPro; IPR006031; XYPPX.
Pfam; PF00191; annexin; 4.
Pfam; PF02162; XYPPX; 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2003 (TrEMBLrel. 23,
                                                             111:1 11 | 1 | 307 GDYRKILLELCG 318
                                                324
                                                                                                                           PRELIMINARY;
                                                313 GDYKKALLLLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 AA;
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID-8090;
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                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEVILLE R.A., Nijjar S., Barnett M.W., Jones E.A.;
Seville R.A., Nijjar S., Barnett M.W., Jones E.A.;
I "Annexin 4 (Xanx-4) has a role in the development of the pronej tubules in Xenopus laevis.";
I tubules in Xenopus laevis.";
I. Submitted (JUN-2201) to the EMBL/GenBank/DDBJ databases.
C -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITIC C -1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
C -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
R EMBL; AY039235; AAK83461.1; -.
R EMBL; AY039235; AAR83461.1; -.
R INTERPIC: IPR001464; Annexin.
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01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                            PRT;
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                            494 GDYKNLLLKLCGSSD 508
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2003 (TrEMBLrel. 23,
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Matches 170; Conservative
                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xer
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                         Annexin 4
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               369 RLGTDESKFNAILCSRSRAHLVAVFNEYQRMTGRDIEKSICREMSGDLEQGMLAVVKCLK 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
EMBL, BC012875; AAH12875.1; -...
INTERFEY: IDR801464; AnnexIn.
                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%; Score 847; DB 11; Length 503; 53.7%; Pred. No. 2.1e-51; ive 59; Mismatches 87; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 AA; 54079 MW; 33F3471EE21A0D32 CRC64;
    Last sequence update)
Last annotation update)
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Last sequence update)
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                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
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GDYRKILLKICGGND 503
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                         Similar to annexin All.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00335; ANX; 4
                                                                                    Mus musculus (Mouse).
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Matches 169; Conserv
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Strausberg R.;
                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
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Q8K2N9
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TLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALL 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 GKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 SSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELKWGTDEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 FITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAE
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White A.H., Wallis G.A.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

-1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

-1- SIMILARITY: CONTAINS 4 ANNEXIN FAMILY.

-1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

EMBL, AF417637; AAL133081.;

InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                 51.3%; Score 840.5; DB 11; Length 327; 57.8%; Pred. No. 3.3e-51; 1.1ve 49; Mismatches 79; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 327;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC030407; AAH30407.1; -. MGD; MGI:1201374; Anxa8.
                                                                                                                                                                                                                                 56DB9CFAFA8C2B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36787 MW; 2EB178E13738CF22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                   327 AA; 36724 MW;
                                                                           InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
BruTs; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                                                                                                              SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
SEQUENCE 327 AA; 36724 MW;
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ProDom; PD000143; Annexin; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00191; annexin; 4.
                                                                                                                                                                                                                                                                                                            Best Local Similarity 57.89
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321 LLSGED 326
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DB 6;

51.0%; Score 836.5;

17

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253
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                                        DLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKO 134
                                                            74 TLKSELSGKFERLIVALMYPPYRYEAKELHDAMKGLGTKEGVIIEILASRTKNQLQEIMK 133
                                                                                            VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 TVKGSPHFNPVPDAETLYKAMKGIGTNEQAIIDVLTRRSSAQRQQIAKSFKAQFGSDLTE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length colbas.";
Mature 420:563-573(2002).
EMBL: AK090055; BAC41070.1; -.
SEQUENCE 323 AA; 36356 MW; 9F69F57BCFAC6A85 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KWGTDEDKFTEVLCLRSFPQLKLTFDEYRNISQKDIEDSIKGELSGHFEDLLLAIVHCAR
                                                                                                                                                   WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                         254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID-10090;
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49.2%; Pred. No. 2.6e-48;
Live 63; Mismatches 97; Indels
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Last annotation update)
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MEDLINE-22354683; PubMed-12466851;
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DYKNALLSLVGSD 326
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Best Local Similarity 49.29
Matches 155; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
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A Cheng W., Taso F.H.C.;

Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

- INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH

INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH

CC IS INVOLVED IN THE BLOOD COAGULATION CASCADE (BY SIMILARITY).

CC I- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MAY FORM

CC I- SIMILARITY: TO OTHER PROTEINS. OF THE ANNEXIN FAMILY.

BEBL; AF012745; AAD01508.1; - - ANDISOR 1; - - SIMILARITY: ANDO1644; Annexin.

BRSP; P13214; IANN.

InterPro; IPR001464; Annexin.

BR FFAM: PF00191; annexin.

PF00019; ANNEXIN.

PRODOM; B000143; Annexin; 4.

PROSITE: PS00123; ANNEXIN; 4.

PROSITE: PS00233; ANNEXIN; 4.

PROSITE: PS00233; ANNEXIN; 4.

PROSITE: PS00233; ANNEXIN; 4.

PROPERA
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                                                                                                      DIKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ 134
                                                                                                                                                             VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 193
                                                                                                                                                                            74
                                                  TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD
                                                                                                                     WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
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                           Gaps
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Oryccolagus cuniculus (Rabbit).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                        Indels
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: 1815B77B6BES0AB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                       84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .68
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           Pred. No. 6.2e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.2%; Score 822.5; DB 55.9%; Pred. No. 6e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                             327 AA.
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                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last seque
01-MAR-2002 (TrEMBLrel. 20, Last annot
Annexin 8 (Annexin 8) (Annexin VIII).
ANXA8 OR ANX8.
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55.9%; FL.
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Best Local Similarity 55.99
Matches 175; Conservative
          Best Local Similarity 55.9
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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270 3
327 AA;
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SEQUENCE
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309 GDYRTVLLKICGEDD 323

Search completed: August 22, 2003, 21:35:25 Job time : 32.6667 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 22, 2003, 21:27:21; Search time 37.6667 Seconds

(without allygaments)

1377.971 Million cell updates/sec

Perfect score: 1642
Sequence: 1642
Sequence: 1 MACGCGHMAQVLRGTVTDFP......KGDTSGDYKKALLLLSGEDD 327

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863
Minimum DB seq length: 200000000

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries
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A_Geneseq_19Jun03:*

1. | SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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24: | SIDS1/gcgdata/geneseqf/geneseqp-embl/AA2002.DAT:*
24: | SIDS1/gcgdata/geneseqf/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
Š.	Score	Match	Match Length DB ID	DB	ID	Description
	1642	100	:	2	i	Modified byman son
0	1630	. 00		5		Modified human ann
1 (**	1630	. 66	327		AAB50864	Modified human and
•	1500	9		i	A N D O O E 1 1	Discorted mandain dim
	0001	9		٠,	********	racental coadulat
יר	OSCT	0.0		?	AAP91933	vascular anti-coag
٥	1590	96.8		12	AAR13082	PAP-I. Homo sapie
7	1590	96.8		20	AAY13923	S65T GFP variant/h
60	1590	96.8		21	AAY84788	Amino acid sequenc
σ	1590	96.8		23		Human annexin V.

anticoagulant PP4 Annexin V/urokinas Annexin V/urokinas PAP-I isolated fro CPB-I. Homo sapie Calphobindin I (CP Human CPB-I protei Sequence vascular Vascular anticoagu CPB-I. Homo sapie	. 14 GFP ASP GFP GFP GFP Can	Human NOVX polypep Human NOVX polypep Human placenta-der S65T GPP variant/h Human cancar assoc Anticoagulative PP Amino acid sequenc Novel human diagno	Annexin XI type I Annexin XI type I Lung cancer associ Human polypeptide Sequence vascular Vascular anti-coag VAC-beta. Synthet Human protein SEQ
AAP90053 AAP2230 AAP22317 AAR26276 AAR41021 ABG32550 AAP80242 AAR11910 AAR11910	AAP91363 AAP1363 AAR13924 AAR13925 AAR7 5695 AAR7 5695 AAR7 66248 AAR8 8393 AAR03725	AAKU3/25 AABU54621 AAR03726 AAY13926 AAB43617 AAP31913 AAY84790 ABG19948	AAR34127 AAR34128 AAY07117 ABP69394 AAP80715 AAP91954 AAR35754
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## ALIGNMENTS

RESULT 1	
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	AAB50865;
XX	
	16-MAR-2001 (first entry)
	Modified human annexin, SEQ ID NO: 6.
KW Huma	Human; annexin; chelation site; nuclear imaging; apoptosis;
	transplant rejection.
XX	
	Homo sapiens.
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	WO200073332-A1.
XX	
	07-DEC-2000.
PF 25-M	25-MAY-2000; 2000WO-US14324.
PR 01-J	01-JUN-1999; 99US-0324096.
	(UNIW ) UNIV WASHINGTON.
××	
PI Tait	Tait JF, Brown DS;
XX	
	WPI; 2001-080465/09.
DR N-PS	N-PSDB; AAC91370,
PT Nove	
	apoprosis, mas n-terminai chetarion site comprising amino actu

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                                                                                                                                                                                   Length 327;
extension which comprises a glycine and a cysteine residue
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                      English.
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                  Page 37-38; 39pp;
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les 327; Conservative
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Pred. No. 1.9e-142;
0; Mismatches 1;
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WPI; 2001-080465/09.
N-PSDB; AAC91368.
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Best Local Similarity
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                             EP279459-A.
JP03219875-A.
           Homo sapiens
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                                                                                                Novel modified annexin useful for imaging vascular thrombi and apoptosis, has N-terminal chelation site comprising amino acid extension which comprises a glycine and a cysteine residue -
                                                                                                                                                                                                                                                                                                         Length 327;
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Pred. No. 1.9e-142;
0; Mismatches 1;
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                                                                    2001-080465/09
                                                Brown DS;
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Best Local Similarity
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10-MAR-2003
12-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                    Recombinant placental coagulation inhibitor - useful for the prevention and treatment of thromboses or disseminated intra-vascular coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                      useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 QAGELKWGTDEEKFITIFGTRSVSHLRKVPDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide exhibits strong anticoagulant activities and is use for the treatment and prevention of e.g. thrombosis or disseminated intravascular coagulation in the brain, heart and peripheral blood vessels, such as cerebral and myocardial infarction. It has no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigenicity against man and can be produced in large amts. using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-2003 to add missing OS field.)
25-MAR-2003 to correct PF field.)
25-MAR-2003 to correct PF field.)
25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.8%; Score 1590; DB 9; 99.7%; Pred. No. 9.3e-139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page ?; ?pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP91953 standard; protein; 320
                                                                                                                                                              Ξ
88EP-0102468
                                           87JP-0037227
87JP-0184428
                                                                                                                                                                Suda
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Matches 319; Conservative
                                                                                                                                                           Saino Y, Iwasaki A,
                                                                                                                                                                                                     WPI; 1988-236733/34.
WPI; 1991-329110/45.
N-PSDB; AAN81113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant methods
                                                                                                                  (KOWA ) KOWA CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 AA;
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K; PBP;

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1 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence, or a fragment of it, is used in the construction of hybrid phospholipid-binding proteins (PBD) comprisaling it least one lipocortin phopholipid binding domain (PBD), e.g. of PAP-1, joined to a gla-domainless vitamin K-dependent protein, e.g. protein C or a crivated protein C. See AAQ12680-81 for such examples. See also AAQ12678-81. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins
and
                                                                                                                                                                                                                 Phopholipid; binding protein; lipocortin; domain; vitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant prodn. of hybrid phospholipid-binding comprising lipocortin phospholipid-binding domain vitamin K-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1590; DB 12;
Pred. No. 9.3e-139;
0; Mismatches 1;
                                                                                                  AAR13082 standard; Protein; 320 AA
           327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 7; 57pp; English.
             KGDTSGDYKKALLLLSGEDD
                        301 KGDTSGDYKKALLLLCGEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.8%;
                                                                                                                                                                                                                                                                                                                              90WO-US07335
                                                                                                                                                                                                                                                                                                                                                     89US-0459082
                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.7
Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                               MPI; 1991-222905/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ12679
                                                                                                                                                                                                                                                       Homo saplens
                                                                                                                                                                                                                                                                                                                              13-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                     29-DEC-1989;
                                                                                                                                                                                                                              gla-domain;
                                                                                                                                                                                                                                                                            409109953-A.
                                                                                                                                                                                                                                                                                                     11-JUL-1991.
                                                                                                                                                 25-MAR-2003
30-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                      Foster DC;
           308
                                                                                                                           AAR13082;
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                                                                         RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This vascular anti-coagulating protein (VAC)-alpha is used in the preparation of monoclonal antibodies (MAbs). The VAC-alpha is injected into a host animal, in conjugation with eak sevice the animal, in conjugation with eak sevice the accordance immunised hosts are then fused with myeloma cells. The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-alpha. Abs can be used as immunossay reagents to detect VAC proteins, as affinity ligands for protein purificm, and as medicaments for binding and/or neutralising VAC proteins in vivo. See also AAN91354 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                     Pascular anti-coagulating proteins; hybridomas; B-cells; myelomas.
                                                                                                                                                                                                                                                                                                                                                                                         Monoclonal antibodies to vascular anti-coagulating proteins - and hybridomas producing such antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1590; DB 10;
Pred. No. 9.3e-139;
0; Mismatches 1;
                                                                                                                                                               1..320
/product=VAC-alpha protein
                                                            Vascular anti-coagulating protein-alpha.
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; fig 1; 11pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.8%;
                                                                                                                                                                                                                                                                                                     (BOEH ) BOEHRINGER INGELHEIM
           (updated)
(updated)
(first entry)
                                                                                                                                                                                                                                                    88DE-3810331
                                                                                                                                                                                                                                                                            88DE-3810331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                             - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-293724/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 AA;
                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN91353
                                                                                                                                                                                                                                                    26-MAR-1988;
                                                                                                                                                                                                                                                                            26-MAR-1988;
          25-MAR-2003
10-MAR-2003
                                  30-JUL-1989
                                                                                                                                                                                                   DE3810331-A.
                                                                                                                                                                                                                            05-OCT-1989
                                                                                                                                                                                                                                                                                                                              Sunther A;
                                                                                                              Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-181465
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Matches
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Rosso MF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2784106-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sanson A,
                                                                                                                                                                                                                                                                                                                             308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY84788;
      89
                                         61
                                                                                 128
                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coating;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
67
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                                                                                                                                                                                                                                                                                                                                                                               GFP; green fluorescent protein; annexin; fusion protein; apoptosis; fluorescent intensity; anionic phospholipid binding affinity; asymmetric distribution; plasma membrane phospholipid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bifunctional fusion protein useful for the detection of apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1590; DB 20;
Pred. No. 9.3e-139;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                            S65T GFP variant/hAnnexin V protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 14-15; 23pp; English.
                                                                                                                                                                                                                       AAY13923 standard; protein; 320 AA
                                                                                                    KGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.8%;
llarity 99.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-US21444
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                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptotic cell detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-277634/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aequorea victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-1998;
                                                                                                                                                                                                                                                                                                    13-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                              AAY13923;
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                                                                                 308
                                                                                                                     301
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Best Local &
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240
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127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phospholipid; antithrombotic; antitumor; antiinflammatory; thrombogenic biomaterial; labelling compound; negative charge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chemical
FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                    FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
                                                                                   ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                      QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemical structure having affinity for phospholipid comprises chemical platform comprising six residues supporting set of chemical functions that are capable of binding to phospholipid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents an annexin polypeptide. The domain cannexin, which may be modified, is used to construct the chemical compounds of the invention. The specification describes chemical compounds which have an affinity for a phospholipid. The chemical compounds which have an affinity for a phospholipid. The chemical compounds comprise at least one chemical platform comprising six residues supporting a set of chemical functions that are capable of binding to the phospholipid and at least partly define the affinity of the structure for the phospholipid. The compounds act as phospholipid sequesters. The compounds are useful for preparing antithrombotic, antitumor and antiniflammatory medicaments, for making coatings for thrombogenic biomaterials, and for preparing labelling compounds useful for analysing and detecting negative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMS ) COMMISSARIAT ENERGIE ATOMIQUE. (UYPA-) UNIV CURIE PARIS VI P & M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       AAY84788 standard; peptide; 320 AA.
                                                                                                                                                                                                                                                                                                 301 KGDTSGDYKKALLLIGGEDD 320
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/note= "domain 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of annexin V.
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                                                                                                                                                                                                                                                                                 KGDTSGDYKKALLLLSGEDD
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deltaV1-5 or their

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29-OCT-1988;
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01-NOV-1989
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                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                              141 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFUIRKEFRKNFATSLYSMI 300
                                                                                                                                          QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV 247
                                                                                                                                                                                                                                                           VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
                                                                                                                                                                       ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 187
                                                                                               8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            damage to
by stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; annexin V; delta RACK; delta protein kinase C; deltaPKC; VI domain; vasotropic; cerebroprotective; deltaVI-1; deltaVI-2; RACK; pseudo-delta receptor for activated C-kinase; deltaVI-5; PKC; protein kinase C; signal transduction; cell growth; gene expression; ion channel activity; translocation; hypoxia; stroke; ischaemic damage; creatine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention discloses peptides comprising deltaV1-1, deltaV1-2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New delta protein kinase C peptide for reducing or enhancing cells or tissues exposed to ischemic or hypoxic event caused or for protecting tissue from damage due to ischemia -
                                            Length 320;
                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human annexin V, containing a delta RACK binding site.
charges on cell surfaces and microvesicles in blood
                                         Score 1590; DB 21;
Pred. No. 9.3e-139;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRD ) UNIV LELAND STANFORD JUNIOR.
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                                                                                                                                                                                                                                                                                                                                                                                ABG31220 standard; Protein; 320 AA.
                                                                                                                                                                                                                                                                                                                 KGDTSGDYKKALLLLCGEDD 320
                                                                                                                                                                                                                                                                                                       KGDTSGDYKKALLLLSGEDD 327
                                        Query Match
Best Local Similarity 99.7%;
Matches 319; Conservative
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                     320 AA;
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                     Sequence
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cell growth, regulation involved in a variety of cellular functions including signal transduction involved in a variety of cellular functions including cell growth, regulation of gene expression and ion channel activity. The localisation of different PKC isozymes to different areas of the cell in turn appears due to binding of the activated isozymes to the specific anchoring molecules (RACKS) Peptides that minic either the PKC-binding site on PKC are isozyme specific translocation inhibitors of PKC. The disclosed peptides are useful in activating or inhibiting translocation or function of deltaPKC. The deltaPKC agonists or antagonists are useful in reducing, enhancing or protecting against damage to cells or tissues due to ischaemic or hypoxic event caused by stroke, Acute administration of the peptides, conjugated to a carrier peptide or a Tat-derived peptide, protected hearts against ischaemic damage as shown by decreased release of creatine kinase. The date indicate that in an intext heart, inhibition of deltaPKC conferred greater than 50% protection against ischaemic damage. The sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.8%; Score 1590; DB 23;
Llarity 99.7%; Pred. No. 9.3e-139;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anticoagulant; PP4 protein; thromboplastin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP90053 standard; protein; 320
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 AA;
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Annexin V, which has high affinity for active thrombocytes, is used as a carrier molecule to build a thrombus trargeting thrombolytic fusion protein. The protein (this sequence) is the result of expression of a fusion gene comprising the Annexin V gene and a low-molecular urckinase gene, in insect cells. The Annexin V-scu-PA-32 fusion protein, expressed in insect cell strain Tn-5B1-4, has high affinity for active thrombocytes and has the fibrinolytic activity of urokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
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                                                                                                                                                                                                                                                             New thrombolytic fusion protein for targetting thrombus – comprises fusion of Annexin V and urokinase % \left( 1\right) =\left\{ 1\right\} =\left\{ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.7%; Score 1587; DB 21; Length 600; 99.4%; Pred. No. 4.3e-138; Live 1; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 2-4; 20pp; Chinese.
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(first entry)
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Best Local Similarity 99.4
Matches 318; Conservative
                                                 Sun J, Yang
                                                                                                                                   2000-413098/36.
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                                                                                                                                                                                N-PSDB; AAA11241
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13-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein; urokinase; insect cell; fibrinolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 320;
                                                                                                                                                                                                                                                    New DNA sequence encoding anticoagulant PP4 protein - and new recombinant protein, vectors, antibodies, etc., useful therapeutically and diagnostically.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of anticoagulant PP4 protein. This inhibits blood coagulation at the thromboplastin stage. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1587; DB 10;
Pred. No. 1.8e-138;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; page 11 and Table 1; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Annexin V/urokinase fusion protein.
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                                                                                     Kupper H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY92930 standard; Protein; 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 96.7%;
Best Local Similarity 99.4%;
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99CN-0113524
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(BEHW ) BEHRINGWERKE AG
                                                                                     Abel KJ,
                                                                                                                                                                  WPI; 1989-166767/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2000
                                                                                     Grundmann U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inidentified
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RESULT 11 AAY92930

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69 GRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                        used within a method which involved adding basic amino acids to it which resulted in its stabilisation. This lead to the production of CPB-I which keeps its activity when it is frozen, molten or has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 319;
                                                                                                                                                                                                           Stabilisation of CPB-1 for drug compsn. - by adding basic aminoacid selected from lysine, arginine and/or ornithine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                         The sequence given is the amino acid sequence of CPB-I.
                                                                                                                                                                                                                                                                                                                                                       processed by several procedures. (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1585; DB 13;
Pred. No. 2.7e-138;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR41021 standard; protein; 319 AA.
                                                                                                                              (KAGA ) KAGAKU OYOBI KESSEI RYOHO.
(KOWA ) KOWA CO LTD.
                                                                                                                                                                                                                                                           Disclosure; Page 2; 4pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                   96.58;
                                                                   90JP-0328286
                                                                                                 90JP-0328286
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Best Local Similarity 99.7'
Matches, 318; Conservative
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                                                                                                                                                                              WPI; 1992-288937/35.
                                                                                                                                                                                                                                                                                                                                                                                                     319 AA;
      JP04198195-A.
                                                                 28-NOV-1990;
                                                                                                 28-NOV-1'990;
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                                    17-JUL-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                           Human proteins having anticoagulant and antiinflammatory activity - isolated from biological fluid by anion-exchange chromatographoc media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 MAQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKŢL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     indicating that PAP-I is probably not constitutively secreted. The Met residue is removed at in a post-translational event and the newly formed NH2-terminal Ala residue is blocked by acetylation. It binds to phospholipid and inhibits phopholipase A2. The protein can substitute heparin or other anticoagulants in the treatment of disseminated intravascular coagulation, deep vein thrombosis, or other disorders. It also has antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPB-1; stabilisation; frozen; molten; processed; activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                         The protein does not contain a leader peptide seguence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ery Match 96.5%; Score 1586; DB 9; st Local Similarity 99.4%; Pred. No. 2.2e-138; tches 318; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                  (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                 Carter BLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                          Disclosure; Page ?; 7pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR26276 standard; protein; 319
 87US-0011782
87US-0059355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                               (ZYMO ) ZYMOGENETICS INC. (UNIW ) UNIV WASHINGTON.
                                                                                             Fujikawa K, Irani MH,
                                                                                                                           WPI; 1988-235049/33
                                                                                                                                                                                                                                                                                                                                                                                                                                 320 AA;
                                                                                                                                             N-PSDB; AANB2107
06-FEB-1987;
05-JUN-1987;
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                                                                                                                                                                                                                                                                                                                                                                                     properties.
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04-FEB-1993
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Best Local 9
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26-FEB-2001; 2001JP-0050297
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                                                                                                                                                                                                                                                                       69 GRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEE 128
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                                                                                                                                                                                                                                                                                                           LRAIKOVYEEEYGSSLEDDVVGDTSGYYORMLVVLLQANRDPDAGIDEAQVEQDAQALFQ
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;
calcium/phospholipid binding protein; polyhydric alcohol.
                                                                                                                            Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I) inhibits protein kinase C (PKC) and is useful in the treatment of mailgnant tumours caused by abnormal activation of PKC. CPB-I is extracted from human or animal organs and may be applied intravenously, orally; intramuscularly, percutaneously or rectally.
                                                                                    Protein kinase C inhibitor effective against malignant tumours contg. (opt. recombinant) calphobindin I
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                                                                                                                                                                                                  Length 319;
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                                                                                                                                                                                                  96.5%; Score 1585; DB 14; 99.7%; Pred. No. 2.7e-138; 1ve 0; Mismatches 1;
                                         (KOWA ) KOWA CO LTD.
(KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKYUSHO
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                                                                                                              Claim 1; Page 2-3; 6pp; Japanese
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       92JP-0019032.
                        92JP-0019032
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                                                                                                                                                                                                            Best Local Similarity 99.7
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human CPB-1 protein
                                                                                                                                                                                  Sequence 319 AA;
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       04-FEB-1992;
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                                                                                                                                                                                                                                                                                                             The invention relates to eye drops contain CPB-I (anexin V) and a polyhydric alcohol having a carbonyl value of not more than 5micro Mol./g. The eyes drops are for treating e.g. corneal diseases. Such eye drops are without unpleasant irritation upon dropping but with satisfactory long-term storage stability. The present sequence is the human CPB-I (calcium/phospholipid binding) protein.
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                                                                                                                                                                  Eye drops for treating e.g. corneal diseases, contain CPB-I and polyhydric alcohol with specific carbonyl value, without unpleasant irritation upon dropping but with satisfactory long-term storability
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Pred. No. 2.7e-138;
0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                     Disclosure; Page 13-14; 16pp; Japanese
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(KOWA ) KOWA CO LTD.
(KAGA ) CHEMO-SERO-THERAPEUTIC
                                                                       Shinoda Y,
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                                                                                                                    WPI; 2002-674988/72
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dsr.09-970-969-6.rsp

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 22, 2003, 21:20:42; Search time 8.66667 Seconds (without alignments) 1774.354 Million cell updates/sec Run on:

US-09-970-969-6 1642 1 MACGCGHMAQVLRGTVTDFP......RGDTSGDYKKALLLLSGEDD 327 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	P08758 homo sapien	P81287 bos taurus	Enm	rati	P17153 gallus gall		homo sa	P14824 mus musculu	P09525 homo sapien		P48037 rattus norv	P97429 mus musculu	P13214 bos taurus	P50994 canis famil	P51901 gallus gall			P33477 oryctolagus		P97384 mus musculu	O35640 mus musculu	P13928 homo sapien	P12429 homo sapien	mus m	P20073 homo sapien	Q07076 mus musculu	P14669 rattus norv	P79134 bos taurus	P26256 hydra atten	Q92125 xenopus lae	P22464 drosophila	P07355 homo sapien	DAA272 hos taurus
SUMMARIES	ļ	qi	ANX5_HUMAN	ANX5_BOVIN	ANXS_MOUSE	ANX5_RAT	ANX5_CHICK	ANX5_CYNPY	ANX6_HUMAN	ANX6_MOUSE	ANX4_HUMAN	ANX4_PIG	ANX6_RAT	ANX4_MOUSE	ANX4_BOVIN	ANX4_CANFA	ANX6_CHICK	ANX4_RAT	ANXB_BOVIN	ANXB_RABIT	ANXB_HUMAN	ANXB_MOUSE	ANX8_MOUSE	ANX8_HUMAN	ANX3_HUMAN	ANX3_MOUSE	ANX7_HUMAN	ANX7_MOUSE	ANX3_RAT	ANX6_BOVIN	ANXC_HYDAT	ANX7_XENLA	ANX9_DROME	ANX2_HUMAN	ANX2 BOVIN
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ď	Query	Match	96.5	93.6	90.1	98.6	77.9	4.99	56.8	56.8	56.2	56.1	56.1	55.8	55.7	54.9	54.6	54.3	52.7	52.6	52.1	51.6	51.2	9.05	48.9	•	47.4	47.3		•	٠.			42.5	42.3
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## ALIGNMENTS

ALIGNMENTS	RESULT 1 ANX5_HUMAN ID ANX5_HUMAN STANDARD; PRT; 319 AA.	01-NOV-1988 (Rel. 09, C 01-NOV-1988 (Rel. 09, L			Homo sapiens (Human). Eukaryota; Metazoa; Chordata;			p SEQUENCE FROM N.A. K MEDLINE-88234495; Pubmed-2967495;		Kuepper H.; "Characterization of ONN prooding human placental	protein (PP4): homology with the lipocortin family.";			MEDLINE=88271329; PubMed=2455636; Mennon-Epons I Bontolingspersor C B M Distance I Bodo G	Stratowa C., Hauptmann R.;		Cazt-uependent phospholipid Eur. J. Biochem. 174:585-59				A Browning J.L., Chow E.P., Burne C., Huang KS., Pratt D., Wachter L.,					<pre>PLDLINE=00103403; FULMEU=2504003; Funakoshi T., Hendrickson L.E., McMullen B.A., Fujikawa K.;</pre>					Mizoguchi T., Sato F., Yoshizaki H., Hirata M., M			
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MEDLINE-91065314; PubMed-2147412;

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TISSUE-Muscle, Ovary, and Skin;

WEDLINE-22388257; PubMed-12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDLINE-22388257; PubMed-12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Batcow K.H., Schaefer C.F., Bhat N.K.,

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                                                                                                                                                       MEDLINE-95047484; PubMed-7958998;
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MEDLINE-89066652; PubMed-2974032;
Biochem. 102:1261-1273(1987).
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analysis at 2.0-A resolution. Implications for membrane binding and
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J. Mol. Biol. 274:16-20(1997).
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D00172; BAA00122.1;
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U01691; AAB40047.1;
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Calcium/phospholipid-binding; Repeat; Blood coagulation;
PROSITE; PS00223; ANNEXIN;
          Annexin; Calcactylation.
INIT_MET
REPEAT
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P48036;
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REPEAT
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                                                                                                                                              LRAIKOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ
                                                                                                                                                                                          AGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVV
                                                                                                                                                                                                      AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A3 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                                  Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOCKIM. BIOPASS. Acta 1160:76-83(1992).

-I-FUNCTION: THIS PROTEIN IS AN ANTICCAGULANT PROTEIN THAT ACTS.
AN INDIRECT INHIBITON OF THE THROMBOLASTIN-SPECIFIC COMPLEX,
WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.

-I-DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

-I-SIMILARITY: GENERAL 4 annexIN FAMILY.

-I-SIMILARITY: CONTAINS 4 annexIN repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Learmonth M.P., Howell S.A., Harris A.C.M., Amess B., Patel Y., Glambanco I., Blanchi R., Pula G., Ceccarelli P., Donato R., Green B.N., Aitken A., "Novel isoforms of CabP 33/37 (annexin V).from mammallan brain: structural and phosphorylation differences that suggest distinct blological roles."
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         Score 1585; DB 1; Length 319;
Pred. No. 1e-95;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                   320 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
MEDLINE-93041974; Pubmed-1420335;
                                                                                                                                                                                                                                                                                               GDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD000143; Annexin; 4.
        Match 96.5%;
Local Similarity 99.7%;
es 318; Conservative
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PRINTS; PR00196; ANNEXIN.
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bovidae; Bovinae; Bos
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P81287;
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                               Matches
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                                                                                                                                                                                                                                                                                                                  LRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                       KSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIK 308
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15-SEP-2003 (Rel. 42, Last sequence update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-1) (Placental anticoagulant protein I) (PAP-1) (PPA)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
                                                                                                                                                                                                              AQVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLF
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                       320;
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                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fernandez
                                                                                                                                    Score 1536.5; DB 1; Length
Pred. No. 1.4e-92;
5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rodriguez-Garcia M.I., Kozak C.A., Morgan R.O., Fernandez
"Mouse annexin V chromosomal localization, cDNA sequence
conservation, and molecular evolution.";
Genomics 31:157(1996).
                                                            ACETYLATION (BY SIMILARITY)
                                                                                                         50FCE18E95F19CB0 CRC64;
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   ANNEXIN 1.
ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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K -> E.
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MEDLINE-96422179; PubMed-8824796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDTSGDYKKALLLL-SGEDD 327
83
155
239
314
1 AC
1 AC
1 25
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8 36
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SEQUENCE FROM N.A.
STRAIN=129/SvJ; TISSUE=Liver;
                                                                                                                                       93.68;
96.68;
                                                                                                                                                     Local Similarity 50.00 ies 309; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                        320 AA;
                                                                                                                                                   Similarity
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RESULT 4
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                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                        -- FUNCTION: THIS PROTEIN IS AN ANTICOAGULANT PROTEIN THAT ACTS AS AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
-- SUBJUNT: MONOMER. BINDS ATRX (By similarity).
-- DOMAIN: A Pair of annexin repeats may form one binding site for calcium and phospholipid.
-- SIMILARITY: BELONGS TO THE ANDEXIN FAMILY.
-- SIMILARITY: CONTAINS 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
MEDLINE-99072820; PubMed-9854034;
Rodriguez-Garcia M.I., Morgan R.O., Fernandez M.R., Bances P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.1%; Score 1479.5; DB 1; Length 319; 93.7%; Pred. No. 6.6e-89;
                                                             Mouse annexin V genomic organization includes an endogenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.6e-89;
9; Mismatches 10; Indels
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ANNEXIN 2.
ANNEXIN 3.
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L; AJ230108; CAA13992.1; JOINED.
L; AJ230111; CAA13992.1; JOINED.
L; AJ230115; CAA13992.1; JOINED.
L; AJ230116; CAA13992.1; JOINED.
L; AJ230118; CAA13992.1; JOINED.
L; AJ230129; CAA13992.1; JOINED.
L; AJ230121; CAA13992.1; JOINED.
L; AJ230122; CAA13992.1; JOINED.
L; AJ230123; CAA13992.1; JOINED.
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94 154 AN
178 238 AN
253 313 AN
319 AA; 35752 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:106008; Anxa5.
InterPro; IPR001464; Annexin.
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                    retrovirus.";
J. Blochem. 337:125-131(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U29396; AAC52530.1; -.
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EMBL, AJ230123; CAA13092.1;
EMBL, AJ230124; CAA13092.1;
HSSP; P14668; 1ABB.
SWISS-2DPAGE; P48036; MOUSE.
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SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                     244 SIPAYLAETLYYAMKGAGTDDHTLIRVVVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 303
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15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipcocrtin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
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STRAIN-Wistar; TISSUE-Brain;
MEDLINE-950301899; PubMed-8667030;
Ohaawa K., Imal Y., Ito D., Kohaaka S.;
"Molecular cloning and characterization of annexin V-binding proteins
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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*Structure of rat annexin V gene and molecular diversity of its
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MEDLINE-93369587; PubMed-8362244;
Concha N.O., Head J.F., Kaetzel M.A., Dedman J.R., Seaton B.A.;
"Rat annexin V crystal structure: Ca(2+)-induced conformational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88273202; PubMed-2968983; Pepinsky R.B., Tizard R., Mattallano R.J., Sinclair L.K., Miller G.T., Browning J.L., Chow E.P., Burne C., Huang K.S., Pratt D., Wachter L., Hession C., Frey A.Z., Wallner B.P.; Frey A.Z., Wallner B.P.; Pitth Alstinct calcium and phospholipid binding proteins share homology with lipocottin I. I., 18101. Chem. 263:10799-10811(1988).
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MEDLINE-96069783; PubMed-7583670;
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                                                                                                                                          313 GDYKKALLLL-SGEDD 327
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ANXAS OR ANXS.
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P14668;
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318 AA;
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ANXA5 OR ANX5.
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Best Local Simi
Matches 291;
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15-SEP-2003
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P17153;
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HELIX
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with highly hydrophilic peptide structure.";
J. Neurochem. 67:89-97(1996).
I. FUNCTION: THIS PROTEIN IS AN ANTICOACULANT PROTEIN THAT ACTS AS AN INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH IS INVOLVED IN THE BLOOD COAGULATION CASCADE.
I. SUBUNIT: MONOMER. Binds ATRX and DNWT1.
I. DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
I. SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
II SIMILARITY: Contains 4 annexin repeats.
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Blood coagulation;
Placenta; Acetylation; 3D-structure.

INIT_MET 0 0 0
REPEAT 20 80 ANNEXIN 1.
REPEAT 92 152 ANNEXIN 2.
REPEAT 176 236 ANNEXIN 3.
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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InterPro; IPR001464; Annexin.
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ProDom; PD000143; Annexin; 4.
                                                                                                                                                              EMBL; M21730; AAA41512.1; -. EMBL; D42137; BAA07708.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                       132 IKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGE
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                                                                                                                                                                           12 LRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRD
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15-5EP-2003 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin I)
(CBP-I) (Placental anticoagulant protein I) (PAP-I) (PP4)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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(Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)
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MEDLINE-88186917; PubMed-2833522;
Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M.,
Deutzmann R., Mollenhauer J., von der Mark R.;
"The structure of anchorin CII, a collagen binding protein isolated
from chondrocyte membrane.";
                                                    ; Score 1455.5; DB 1; Length 318;
; Pred. No. 2.3e-87;
12; Mismatches 13; Indels 1;
35613 MW; 1A755A7C11FA11CE CRC64;
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Moss S.E., Crumpton M.J.;
"Alternative splicing or cloning artefact?";
Trends Blochem. Scl. 14:325-325(1989).
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STANDARD;
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321 AA;
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Matches 250; Conserv
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 NCBI_TaxID=8330;
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P70075:
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SEQUENCE
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             MEDLINE-90243721; PubMed-2159478; Fernandez M.P., Selmin O., Martin G.R., Yamada Y., Pfaeffle M., Deutzmann R., Mollenhauer J., von der Mark K.; artucture of anchorin CII, a collagen binding protein isolated from chondrocyte membrane."; J. Blol. Chem. 265:8344-8344(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | V. PAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
| MEDLINE-93229489; PubMed=8471604;
| MEDLINE-93229489; PubMed=8471604;
| Bewley M.C., Boustead C.M., Walker C.M., Waller C.M., Huber R.;
| Belochemistry 32:3923-3929(1993).
| Function: Colladgen BinDing PROTEIN.
| FUNCTION: Colladgen BinDing PROTEIN.
| DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
| SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
| SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-White leghorn; TISSUE-Liver;
STRAIN-White leghorn; TISSUE-Liver;
MEDLINE-94215900; PubMed-8163186;
Fernandez M.P., Fernandez M.R., Morgan R.O.;
"Structure of the gene encoding anchorin CII (chick annexin V).";
Gene 141:179-186(1994).
                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-LIVET;
MEDLINE-92249384; PubMed-8484740;
MEDLINE-92249384; PubMed-8484740;
MEDLINE-91249384; PubMed-8484740;
MISOLATION, Characterization and localization of annexin V from chicken liver.";
Biochem. J. 291:601-608(1993).
                                                                                                                                               REVISIONS.
Pfacfile M., Ruggiero F., Hofmann H., Fernandez M.P., Selmin O. Yamada Y., Garrone R., von der Mark K.;
EMBO J. 9:1336-1336(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calcium/phospholipid-binding; Repeat; 3D-structure.
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.*
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AAB39917.1; JOINED.
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SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
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Pfam; PF00191; annexin; 4.
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EMBL, U01671, AAB39917.1; JO
EMBL, U01672, AAB39917.1; JO
EMBL, U01673, AAB39917.1; JO
EMBL, U01675, AAB39917.1; JO
EMBL, U01676, AAB39917.1; JO
EMBL, U01678, AAB39917.1; JO
EMBL, U01678, AAB39917.1; JO
EMBL, U01678, AAB39917.1; JO
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PDB; 1ALA; 31-OCT-93.
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                                                                                                                     ELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALF
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 42, Last annotation update)
Annexin A5 (Annexin V).
Cynops pyrrhogastra (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yammanoto T., Hikono T., Abe S.I.; "Differential expression of annexin V during spermatogenesis in the newt Cynops pyrrhogaster."; Dev. Genes Evol. 206:64-71(1996).
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                                          Length 321;
                                                                                 Indels
36198 MW; 43E2983F86797025 CRC64;
                                     77.9%; Score 1279; DB 1; ilarity 78.1%; Pred. No. 6.1e-76; Conservative 38; Mismatches 32;
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QKDTSGDYRKALLLLCGGDD 320
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us-09-970-969-6.rsp

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[1]
SEQUENCE FROM N.A.
                                            Crumpton M.J.;
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                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                         61 SAAFKTLFGRDLLDDLKSELTGRFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEI
                                                                                                                                                                                                                                                                                                                                                         Gaps
          MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY). DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1988 (Rel. 08, Created)
15-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annottation update)
Annexin A6 (Annexin VI) (Lipcortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                   DB 1; Length 323;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                     182 242 ANNEXIN 3.
257 317 ANNEXIN 4.
323 AA; 35981 MW; 044B31AC28164CE2 CRC64;
                                                                                                                                                                                                                                                                                                                                 66.4%; Score 1089.5; DB 1; 66.7%; Pred. No. 1.1e-63; iive 45; Mismatches 59;
                              calclum and phospholipid.
-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-1- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                      Annexin; Calcium/phospholipid-binding; Repeat.
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ANNEXIN 3.
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
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PROSITE; PS00223; ANNEXIN; 4.
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242
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Matches 218; Conserv
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P08133;
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Attachal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Attachal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Datchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Datchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Datchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Datchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carvinci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Schergren E.J., Lu X., Gibbs R.A.,

RA Whiting M.M., Schergren E.J., Lu X., Gibbs R.A.,

RA Blakesley R.W., Touchman J.W., Scheurtz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length

RY human and mouse CDNA sequences.";

R. human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-88124902; PubMed-2963335,
Suedhof T.C., Slaughter C.A., Leznicki I., Barjon P., Reynolds G.A.;
"Human 67-kDa calelectrin contains a duplication of four repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S:
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-!- MISCELLANDEDUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: CONTAINS 8 ANNEXIN FE

    -!- DOMAIN: A pair of annexin repeats may form one binding site for
calcium and phospholipid.

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-!- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF CA(2+) FROM INTRACELLULAR STORES.
-!- INDUCTION: BY EBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Iwasaki A., Suda M., Watanabe M., Nakao H., Hattori Y., Nagoya T.,
Saino Y., Shidara Y., Maki M.;
Siructure and expression of CDNA for calphobindin II, a human
placental coaqulation inhibitor.";
J. Biochem. 106:43-49(1989).
                                         Crompton M.R., Owens R.J., Totty N.F., Moss S.E., Waterfield M.D.,
                                                                                                                                  structure of the human, membrane-associated Ca2+-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96326697; PubMed-8709144;
Benz J., Bergner A., Hofmann A., Demange P., Goettig P., Liemann Huber R., Voges D.;
"The structure of recombinant human annexin VI in crystals and membrane-bound.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yoshizaki H., Mizoguchi T., Arai K., Shiratsuchi M., Shidara Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Structure and properties of calphobindin II, an anticoagulant protein from human placenta."; J. Biochem. 107:43-50(1990).
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                                                                                                                                                                                protein p68 a novel member of a protein family.";
EMBO J. 7:21-27(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found in 35-kDa lipocortins.";
Proc. Natl. Acad. Sci. U.S.A. 85:664-668(1988)
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MEDLINE-89380132; PubMed-2528541;
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MEDLINE=90236978; Pubmed=2139657;
MEDLINE-88196081; PubMed-3258820;
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                                                                                                                                                                                   PROSITE; PS00223; ANNEXIN; 8.
Annexin; Calcium/phospholipid-binding; Repeat; Acetylation;
Phosphorylation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                               ; Score 932; DB 1; Length 672;
; Pred. No. 4e-53;
52; Mismatches 80; Indels
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S -> T (IN REF. 2).
E -> D (IN REF. 1).
2829237029BDIDCB CRC64;
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 5.
ANNEXIN 6.
ANNEXIN 7.
ANNEXIN 9.
ACETYLATION.
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P14824;
01-APR-1990 (Rel. 14, Created)
                                                                                                                                       InterPro; IPR001464; Annexin. Pfam: PF00191; annexin; 8. PRINTS; PR00196; ANNEXIN. ProDom; PD000143; Annexin; 8.
                                                                                                                                                                                                                                                                                                                               75742 MW;
                                                                    EMBL; D00510; BAA00400.1; -. EMBL; Y00097; CAA68286.1; -. EMBL; J03578; AAA35656.1; -. EMBL; BC017046; AAH17046.1; -.
                                                                                                                                                                                                                                                                                                                                               56.8%;
58.1%;
                                                                                             EMBL; BC017046; AAH17046.1;
PIR; JU0032; AQHU6B.
PDB; 1M91; 07-AUG-02.
Genew; HGNC:544; ANXA6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDYKKALLLLSGEDD 327
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                                                                                                                                                                                                                                                                                                                                                                183; Conservative
                                                                                                                                                                                                                              160
244
319
431
503
592
667
                                                                                                                                                                            SMART; SM00335; ANX; 8
                                                                                                                                                                                                                                                                                             1
225
554
618
672 AA;
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                            MOD_RES
CONFLICT
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Best Local
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ANX6_MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL 72
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                                                                                                                                                                                                                                                                                                                                                                                  LEUR. J. Blochem. 177:21-27(1988).
-!- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE OF CA(2+) FROM INTRACELLULAR STORES.
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-!- MISCELLAMBOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY: SIMILARITY: COntains 0 annexin repeats.
01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II)
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                   Moss S.E., Crompton M.R., Crumpton M.J.; "Molecular cloning of murine p68, a Ca2+-binding protein of lipocortin family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00335; ANX; 8.
PROSITE; PS00223; ANNEXIN; 8.
Annexin; Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 4e-53; 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.8%; Score 932;
59.0%; Pred. No. 4
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ANNEXIN 2.
ANNEXIN 4.
ANNEXIN 6.
ANNEXIN 6.
ANNEXIN 7.
ANNEXIN 7.
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MGD; MGI:88255; Anxa6.
InterPro: IPR001464; Annexin.
Pfam; PR00191; annexin; 8.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
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PIR; S01786; S01786.
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16; Conservative
                                                                                                                           Mus musculus (Mouse).
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532
607
672 AA;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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100
184
259
371
                                                                                                  ANXA6 OR ANX6.
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Best Local Simi
Matches 186;
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RR TYSSUE-2388257; PubMed-12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

RA Rhey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Schmitz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Scheln J.E., Jones S.J.M., Marra M.A.;

R Generation and Initial analysis of more than 15,000 full-length
                           190 KWGTDEAQFIYILGNRSKQHLRLVFDEYLKTTGKPIEASIRGELSGDFEKLMLAVVKCIR 249
                                                                                                                                                                                    ANX4_HUMAN STANDARD; PRT; 318 AA.
P09525; Q9663; Q9683; Q98MX1;
01-MAR-1989 (Rel. 10, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annottation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
(PPOTEIN II) (P32.5) (Placental anticoagulant protein II) (PAP-II)
(PPA *X) (35-beta calcimedin) (Carbohydrate-binding protein P33/P41)
ANXA4 OR ANX4.
                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-8830902; PubMed-2970257; Grundmann U., Amann E., Abel K.-J., Kuepper H.A.; Grundmann U., Amann E., Abel K.-J., Kuepper H.A.; Istolation and expression of cDNA coding for a new member of the phospholipase A2 inhibitor family "; Behring Inst. Mitt. 82:59-67(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97239215; PubMed-9084877;
Satoh A., Takayama E., Kojima K., Ogawa H., Katsura Y., Kina T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of human p33/41 (annexin IV), a Ca2+ dependent carbohydrate-binding protein with monocional anti-annexin IV antibodies, ASI1 and ASI7."; Biol. Pharm. Bull. 20:224-229(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92155721; Pubmed-1346776;
Tait J.F., Smith C., Frankenberry D.A., Miao C.H., Adler D.A.,
Disteche C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Chromosomal mapping of the human annexin IV (ANX4) gene."; Genomics 12:313-318(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
                                                                                    327
                                                                                                   |:|||||| | | ||
310 GEYKKALLKLCGGDD 324
                                                                                    GDYKKALLLISGEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
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                                                                                                                                                                          "Sedimentation equilibrium analysis of five lipocortin-related phospholipaes A2 inhibitors from human placenta. Evidence against a mechanistically relevant association between enzyme and inhibitor."; J. Biol. Chem. 263:18657-18663(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY. -!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY. -!- SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human placental annexin IV.";
J. Mol. Biol. 216:219-221(1990).
-!- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
-!- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
                                                                                                                  Ahn N.G., Teller D.C., Bienkowski M.J., McMullen B.A., Lipkin E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY.

MEDLINE-24073383; PubMed-2254922;
Freemont P.S., Diessen H.P.C., Verbi W., Crumpton M.J.;
"Crystallization and preliminary X-ray crystallographic studies of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                comparative
                                                                                                                                                                                                                                                                                                                                                                                   Tait J.F., Sakata M., McMullen B.A., Miao C.H., Funakoshi
Hendrickson L.E., Fujikawa K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characterization four members of the lipocortin family.";
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16B19E01500350F7 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                "Placental anticoagulant proteins: isolation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2e-53;
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InterPro: IPR001464; Annexin.
Prim: PF00191; annexin; 4.
ProDom: PD000143; Annexin; 4.
SMART; SM00335; ANX; AN; ANSOSTE; PS00223; ANXENIN; Annexin; 4.
Annexin; Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-14; 27-71; 99-143 AND 280-318.
MEDLINE=89118212; PubMed=2975506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Mismatches
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
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                           [5]
SEQUENCE OF 26-55; 98-123 AND 279-307.
MEDLINE-8906652; PubMed-2974032; Rankowski M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M19383; AAC41689.1; ALT_INIT.
EMBL; M82809; AAA51740.1; -.
EMBL; D78152; BAA11227.1; ALT_INIT.
EMBL; BC001182; AAH00182.1; ALT_INIT.
EMBL; BC011659; AAH11659.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 27:6268-6276(1988).
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58.3%;
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SWISS-2DPAGE; P09525; HUMAN.
PMMA-2DPAGE; P09525; -
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Best Local 9
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                                                                       193
                                                                                      ANX4_PIG STANDARD; PRT; 318 AA.
P08132; Q29306;
D1-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-1988 (Rel. 08, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
(Protein II) (P32.5) (Placental anticoagulant protein I) (PAP-II)
ANX4 OR ANX4.
                            |||||| ||:|: :|: :|| |||:| || ||::| ||||:| |||:| |||:|| |||:|| ||:|| ||-||:|| ||-||:|| ||-||:|| #GTDEVXFLIVECMRN
            DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK
                                                                     OVYEEPYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELK
                                                                                                                                WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                     IPAYLAETLYYAMKGAGTODHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Intestinal epithelium;
MEDLINE-87275850; PubMed-2956093;
Weber K., Johnsson N., Plessmann U., Van P.N., Soling H.-D., Ampe C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SDBUNIT: Moncomer.
-1- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-1- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.
-1- SIMILARITY: BELLONGS TO THE ANNEXIN FAMILY.
-1- SIMILARITY: CONTAINS 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The amino acid sequence of protein II and its phosphorylation site for protein kinase C; the domain structure Ca2+-modulated lipid binding proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Small intestine;
MEDLINE=96327607; Pubmed=8672129;
Winteroe A.K., Fredholm M., Davies W.;
Winteroe A.K., Fredholm M., Davies W.;
"Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones.";

"Ibrary: analysis of 839 clones.";

Ammen. Genome 7:509-517(1996).

"Involve MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; F14682; CAA23194.1; -.
                                                                                                                                                                                                                                                               327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
42, Last annotation update)
64, Chnexin A6 (Annexin A1) (Lipocortin VI) (P68) (P70) (Protein III)
64, Canculum-binding protein CATA 65/67).
ANXA6 OR ANX6.
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-!- FUNCTION: MAY ASSOCIATE WITH CD21. MAY REGULATE THE RELEASE
                                                                                                               PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat; Phosphorylation;
Activation 0 0
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                                                                                                                                                                                                                                                                                                                                                     Length 318;
                                                                                                                                                                                                                                                                                                                                                 Query Match 56.1%; Score 921; DB 1; Length 31 Best Local Similarity 58.6%; Pred. No. 8.3e-53; Matches 184; Conservative 51; Mismatches 79; Indels
                                                                                                                                                                                                                                                                      1 1 ACETYLATION (PROBABLE).
6 6 PHOSPHORYLATION (BY PKC).
318 AA; 35697 MW; FA7D9CE2B7C631E8 CRC64;
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ANNEXIN 2.
ANNEXIN 3.
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MEDLINE-95331313; Pubmed-7607247;
                  InterPro; IPR001464; Annexin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 DYKKALLLLSGEDD 327
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305 DYRKVLLILCGGDD 318
                                                      PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin;
SMART; SM00335; ANX; 4.
                                    Pfam; PF00191; annex1n; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
P13214; 1ANN
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                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab.ch).
                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                           Gaps
CA(2+) FROM INTRACELLULAR STORES.

DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.

MISCELLAMEDOS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY.

SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

SIMILARITY: Contains 8 annexin repeats.
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                                                                                                                                                                                                                                                                                                                                                                       Length 672;
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                                                                                                                                                                                                                                                       BY SIMILARITY.

ANNEXIN 1.

ANNEXIN 3.

ANNEXIN 4.

ANNEXIN 6.

ANNEXIN 7.

ANNEXIN 7.

ANNEXIN 8.
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Pred. No. 2.1e-52;
                                                                                                                                                                                                               ProDom; PD000143; Annexin; 8.
SMART; SM00332; ANX; 8.
SMO0321E; PS00223; ANNEXIN; 7.
Annexin; Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         48; Mismatches
                                                                                                                                                                                                                                                                                                                                                   75622 MW;
                                                                                                                                                  EMBL; X86086; CAA60040.1; -. PIR; S65683; S52844. HSSP; P79134; IAVC. InterPro; IPR001464; Annexin.
                                                                                                                                                                                         Pfam; PF00191; annexin; 8.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
                                                                                                                                                                                                                                                                                                                                                                      56.1%;
58.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDYKKALLLLSGEDD 327
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310 GEYKKALLKLCGGDD 324
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 58.7 Matches 185; Conservative
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244
319
431
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503
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532
607
672 AA;
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P97429;
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Best Local 8
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ID ANX4_M
AC P97429
DT 01-NOV
DT 28-FEB
DE Annexii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
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                                                                                                                                                                    Sable C.L., Shannon J., Riches D.W.H.;
Submitted (JAN-1997) to the EMBL/Genbank/DDBJ databases.
-1-FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PRONOTES
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
-1-DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
-1-MISCELLANBOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY (BY SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-1-SIMILARITY: COntains 4 annexin repeats.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53FAC7AD8006BC0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.8%; Score 916; DB 1; 57.3%; Pred. No. 1.8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY
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ANNEXIN 3.
ANNEXIN 4.
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Annexin; Calcium/phospholipid-binding;
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154 AN
238 AN
313 AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:88030; Anxa4.
InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
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ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U72941; AAB40697.1; -. HSSP; P13214; 1ANN.
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94 1
178 2
253 3
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                                                                                                    [1]
SEQUENCE FROM N.A.
STRAIN-C3H/HeJ;
                                                                          NCBI_TaxID-10090;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin I) (Chromobindin 4)
(Protein II) (P22.5) (Placental anticoagulant protein II) (PAP-II)
(PP3-X) (35-beta calcimedin) (Carbohydrate-binding protein P33/P41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **ATA CRYSTALLOGRAPHY (3 ANGSTROMS).
**ATA CRYSTALLOGRAPHY (3 ANGSTROMS).
**MEDLINE-98070213; PubMed-9445281;
**Banotti G., Malpeli G., Gliublch F., Folli C., Stoppini M., Olivi L.,
Savoia A., Berni R.;
**Structure of the trigonal crystal form of bovine annexin IV.";
**Biochem. J. 329:101-106(1998).
**I- SUBUNIT: Monomer.
**I- DOMAIN: A pair of annexin repeats may form one binding site for calcium and phospholipid.
**I- SUBUNIT: MISCELLANEOUS: SEEMS TO THE ANNEXIN FAMILY.
**I- SIMILARITY: COLTAINS 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

MEDLINE=96205957; PubMed=8631806;

KOjima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;

Kojima K., Yamamoto K., Irimura T., Osawa T., Ogawa H., Matsumoto I.;

"Characterization of carbohydrate-binding protein p33/41: relation

with annexin IV, molecular basis of the doublet forms (p33 and p41),

and modulation of the carbohydrate binding activity by

phospholipids.";

J. Blol. Chem. 271:7679-7685(1996).
                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                  TISSUE-Liver;

BUDIINE-89050089; PubMed-2847715; Annuan H.C., Gaffey L.C., Lynch K.R., Creutz C.E.; Cloning and characterization of a cDNA encoding bovine endonexin
                                                                                                                                                                                                                                                                                                                                              (chromobindin 4).";
Biochem. Biophys. Res. Commun. 156:660-667(1988).
                          318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sutton R.B., Sprang S.R.,
Submitted (SEP-1995) to the PDB data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                          PRT;
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PIR; A31578; LUBO4.
PDB; 1ANN; 29-JAN-96.
PDB; 1AOW; 14-JAN-96.
PDB; 1143; 25-PRF-01.
InterPro; IPRO01464; Annexin.
Pfam; PF00191; annexin; 4.
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ProDom; PD000143; Annexin; 4.
SMART; SM00335; ANX; 4.
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                          STANDARD;
                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                            ANXA4 OR ANX4.
                         ANX4_BOVIN
P13214;
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DDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIK 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 IPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG 313
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 41, Last sequence update)
Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule membrane associated protein) (ZAP36).
ANXA4 OR ANX4.
Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                              ;
0
Annexin; Calcium/phospholipid-binding; Repeat; 3D-structure,
                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.7%; Score 914; DB 1; Length 318; Best Local Similarity 58.0%; Pred. No. 2.4e-52; Matches 182; Conservative 51; Mismatches 81; Indel8
                                                                                                                                                                                                                                                                                                                                                   35757 MW; 86BDBDF349D774FD CRC64;
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304
318 AA;
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P50994;
          INIT_MET
REPEAT
REPEAT
REPEAT
CONFLICT
CONFLICT
HELIX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVLRGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFG
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                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
(Chromobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).
ANXA6 OR ANX6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 671;
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57.7%; Pred. No. 7.9e-51;
ilve 51; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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ANNEXIN 2.
ANNEXIN 3.
ANNEXIN 4.
ANNEXIN 5.
ANNEXIN 6.
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Annexin; Calcium/phospholipid-binding; REPEAT 27 87 ANNEXIN 1.
REPEAT 183 243 ANNEXIN 3.
REPEAT 183 243 ANNEXIN 3.
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HSSP; P79134; 1AVC.
InterPro; IPR001464; Annexin.
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 8.
SMART; SM00335; ANX; 8.
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                                                                                                                                          Gallus gallus (Chicken)
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258
370
442
531
607
671 AA;
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=9031;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CALCIUM/PHOSPHOLIPID-BINDING PROTEIN WHICH PROMOTES MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
-I- DOMAIN: A pair of annexin repeats may form one binding site for
                                                                                                                                                                                                                calcium and phospholipid.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42EF5B89179B4863 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Score 901; DB 1;
57.0%; Pred. No. 1.6e-51;
Live 54; Mismatches 81;
                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE ANNEXIN FAMILY. SIMILARITY: Contains 4 annexin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   671 AA.
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ANNEXIN 1.
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ANNEXIN 3.
ANNEXIN 4.
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                                                                               SEQUENCE FROM N.A.
STRAIN-Mongrel; TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN; 4.
ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D38223; BAA07398.1; -. HSSP; P13214; 1ANN.
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DYRKVLLILCGGDD 318
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es 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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238
313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 2
253 3
318 AA;
                                                                                                                                                                                                                                                          (BY SIMILARITY)
                                      NCBI_TaxID-9615;
                                                                                                                    Fukuoka S.-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANX6_CHICK
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69 65

Gaps

1;

Search completed: August 22, 2003, 21:33:39 Job time : 9.66667 secs

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090955 drosophila

08wp09 bombyx mori

08wp09 bombyx mori

087512 caenorhabdi

09ng6 bombyx mori

09160 bombyx mori

09693 drosophila

08tbv2 homo sapien

09czi7 mus musculu

095v57 artemia san

099193 mus musculu

089193 mus musculu

089494 drosophila

093446 oryzias lat

09vxg4 drosophila

093476 boryzias lat

09vxg4 drosophila
                                                                                                                                                                                                                                                                                              Q92128 xenopus lae
Q27864 caenorhabdi
Q8ccv9 mus musculu
Q8bsl2 mus musculu
Q27473 caenorhabdi
Q9xy89 schistosoma
                                                    0921d0 mus musculu
  Q8vin2 rattus norv
                          09n161 bombyx mori
081g18 drosophila
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                                                                                                                                                                                                                                                                                    Q8hzm6 equus cabal
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
C. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
C. DOLCIUM AND PHOSPHOLIPID (BY SIMILARITY).
C. I- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
C. I- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
C. I- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
C. I- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
C. I- SIMILARITY: CONTAINS 4 ANNEXIN.
C. I- SIMILARITY: CONTAINS 4 ANNEXIN.
C. I- SIMILARITY: MAH18671.1;
C. I- SIMILARITY: MAH18671.1;
C. I- SIMILARITY: ANNEXIN.
C. I- SIMILARITY: MAH18671.1;
C. I- SIMILARITY: ANNEXIN.
C. I
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1585; DB 4;
Pred. No. 1.2e-103;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 AA
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090XG4
098SH7
098IZM6
092128
027864
08CCV9
                                    Q81GJ8
Q921D0
Q9NL59
Q9NG55
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Q95V57
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Q8MJB5
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Q8WPH0
Q27512
Q9GNG6
Q9NL60
Q969D3
Q8TBV2
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Best Local Similarity 99.4%;
Matches 318; Conservative
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 TISSUE-Skin;
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Query Match
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Q8WV69;
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                                                                                 August 22, 2003, 21:29:22 ; Search time 31.6667 Seconds (without alignments) 2664.733 Million cell updates/sec
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                                                                                                                                    US-09-970-969-6
1642
1 MACGCGHWAQVLRGTVTDFP......KGDTSGDYKKALLLLSGEDD 327
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O70371 ratt
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            version 5.1.6
- 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                            - protein search, using sw model
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_unclassified:*
          GenCore
Copyright (c) 1993
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Maximum DB :
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302 AA
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MEDLINE-99262163; PubMed-10329451;
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                                                                                                                                             GDYKKALLLCGGEDD 319
                                                                                                                         313 GDYKKALLLL-SGEDD 327
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07,
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01-AUG-1998 (TrEMBLrel. 0'
01-AAR-2003 (TrEMBLrel. 2'
Lipocortin V (Fragment).
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxIb=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SITE
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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L Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

C -1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE

CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

C -1- SIMILARITY: BELONGS TO THE ANNEXIN REPEATS.

C -1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

REMBL; BCIO03716.1; -.

DR HSSP; P14668; IA8B.

MGD; MGI:106008; Anxa5.

DR InterPro: IPRO01464; Annexin.

DR PRINTS; PRO0196; ANNEXIN.

DR PRINTS; PRO0196; ANNEXIN.
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Last sequence update)
Last annotation update)
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Local Similarity 93.4%; Pred. No. 5.8e-96;
les 295; Conservative 9; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                    KGDTSGDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                       319 AA; 35738 MW;
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72 LLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRA 131
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                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.7%; Score 1390; DB 11; Length 302; 92.0%; Pred. No. 5.6e-90; tive 12; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 302
302 AA; 33965 MW; AB9FB40934A3D007 CRC64;
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Last sequence update)
Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-JUN-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
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Osterloh D., Wittbrodt J., Gerke V.;
Characterization and developmentally regulated expression of four annexins in the Killiffish medaka.";
DNA Cell Biol. 17:835-847(1998).
-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN FRAMILY.
-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.
EMBL; Y11553; CAA72123.1; -.
INTERPRO; IPR001464; Annexin.
                                                                                                                                                                        Oryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Meopterygii, Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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(TrEMBLrel. 23, Last sequence update)
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64.4%; Pred. No. 1.8e-65;
1ve 48; Mismatches 62
                                                        317 AA.
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PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
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                                                                                       01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2003 (TrEMBLrel. 23, Annexin max2.
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73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
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MEDLINE-223546B3: PubMed-12466B51;
The FANTOM Consortium.
The FANTOM Consortium.
The FANTOM Consortium.
The FANTOM Consortium.
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conns.";
Nature 420:563-573(2002)
EMBL: AK010342: BAC25291.1;
SEQUENCE 476 AA; 53669 MW; 9390C5B5E6653D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
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Submitted (Apr-201) to the EMBL/GenBank/DDBJ databases.
Submitted (Apr-201) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
-!- SIMILARITY: COUTAINS 8 ANNEXIN REPEATS.
-!- SIMILARITY: COUTAINS 8 ANNEXIN REPEATS.
--- HSSP: P79114; 1AVC.
--- MGD; MGISS5; ARA65.
--- MGD; MGISS5; ARA66.
--- MGD; MGISS5; ANNEXIN.
--- FROUSTS TO THE ANNEXIN TO THE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                           Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.8%; Score 932; DB 11, 59.0%; Pred. No. 1.8e-57, iive 48; Mismatches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        667
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Mus musculus (Mouse),
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|||||| | | ||
311 GEYKKALLKLCGGDD 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 GDYKKALLLLSGEDD 327
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17,
23,
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Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
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annotation
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                     PROSITE; PS00223; ANNEXIN; 8.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                           667;
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                                                                                                                                                                                             80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420.565-573(2002).
EMBL: AK030728: BACZ7101.1; -.
SEQUENCE 673 AA; 75885 MW; DCC5FC56CBD88809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Indels
                                                                                                                                                           Length
                                                                                                                 667 AA; 75260 MW; 363088A2A55CFF34 CRC64;
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Last sequence update)
Last annotation update)
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4.1e-57;
                                                                                                                                                     ; Score 932; DB 11;
; Pred. No. 2.9e-57;
49; Mismatches 80
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59.0%; Pred. No. 4.1e
ilve 48; Mismatches
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MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
                   PD000143; Annexin; 8.
                                                                                                                                                       56.8%;
59.0%;
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23,
                                                                                                                                                                                             Conservative
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                                     SMART; SM00335; ANX; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                       Best Local Similarity
Matches 186; Conserv
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                                                                                                                                                       Match
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Matches
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  KOVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL
                                                                                     KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                        SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 AEDLSSELSGHFQSVVLGLLMPAPVYDAYELKAAMKGAGTEEACLIDILASRSNSEMNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neoprerygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyldae; Oryziinae; Oryzias.
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SWART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99025617; PubMed-9809745; MEDLINE-99025617; PubMed-9809745; Osterloh D., Wittenord J., Gerke V.; Osterloh D., Wittenord J., Gerke V.; Characterization and developmentally regulated expannexins in the killifish medaka."; DNA Cell Balol. 17:835-847 (1998).

-1- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

-1- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

EMBL; Y11252; CAA72122.1; -

HSSP; P13214; IANN.
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Oryzias latipes (Medaka fish) (Japanese ricefish).
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Best Local Similarity 54.5%; Pred. No. 4.5e-53;
Matches 170; Conservative 59; Mismatches 83
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ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                                                                                                                      |:|||||| | || GEYKKALLKLCGGDD 325
                                                                                                                                                                                                                                                           GDYKKALLLLSGEDD 327
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                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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133
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                                                                                                            090X16;
                                                                                            090X16
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                                                                  RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                           KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps.
                                                                                                                                                                                                                                                                                                                                                                                               annexins in the killifish medaka.";

DNA Cell Biol. 17:835-847(1998).

-!- DOMAIN: A PAIR OF ANNEXIN REPEATS MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.

-!- SIMILARITY: CONTAINS 4 ANNEXIN REPEATS.

EMBL; Y11255; CAA72125.1; -.

InterPro; IPR001464; Annexin.

InterPro; IPR006331; XYPPX.
                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99025617; PubMed-9809745;
Osterloh D., Wittbrodt J., Gerke V.;
"Characterization and developmentally regulated expression of four
                                                                                                                                                                                                                               Annexin max4.
Oryzlas latipes (Medaka fish) (Japanese ricefish).
Bukaryota: Metazoa: Chordata; Cranlata; Vertebrata; Euteleostomi;
Bukaryota: Metazoa: Chordata; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianlchthyidae; Oryzlinae; Oryzlas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium: Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.1%; Score 856; DB 13; Length 508; 55.2%; Pred. No. 4.4e-52; tive 51; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      508 AA; 53051 MW; 3C6728D475CAE430 CRC64;
                                                                                                                                                                                                       (TrEMBLrel. 08, Last sequence update) (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                          Created)
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00191; annexin; 4.
Pfam; PF02162; XYPPX; 15.
                                                                 GDYKKALLLLSG 324
                                                                              Conservative
                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00335; ANX; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 174; Conserv
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                    247
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KGTIKPYPNFNAADDVQKLRNAMKGAGTDEDAVIDVIANRTLSQRQEIKTAYKTTVGKDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 LDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SWART; SM00335; ANX; 4.
PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5C28CAFAC17687D CRC64;
                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.7%; Score 849; DB 13;
54.0%; Pred. No. 7.1e-52;
ive 55; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
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                                                                             321
                                                                                                         Created)
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                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35801 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDYKNLLLKLCGSSD 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDYKKALLLLSGEDD 327
                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 54.09
Matches 170; Conservative
                                                                             PRELIMINARY;
                                                                                                                                                                                                          Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 AA;
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=8355;
                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193
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                                                                                                                                                    Annexin 4
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        494
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Q921F1;
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Annexin VIII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
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                                                                                                                                                                                                                                                                                                                                         SRAYKTEFQKTLEEAIRSDTSGHFQRLLISLSQGNRDESTNVDMSLVQRDVQELYAAGEN 368
                                                                                                                                                                                                                                                                                                                                                                 KQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGEL 192
                                                                                                                                                                                                                                                                                                                                                                                                    193 KWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIR 252
                                                                                                                                                                                                                                                                                                                                                                                                              : |||| || | :|| :|| || :|| || ::
RLGTDESKFNAILCSRSRAHLVAVFNEYQRWTGRDIEKSICREMSGDLEQGMLAVVKCLK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                            13 RGTVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDL 72
                                                                                                                                                                                                                                                                           Gaps
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                           PROSITE; PS00223; ANNEXIN; 4.
Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                       51.6%; Score 847; DB 11; Length 503; 53.7%; Pred, No. 1.9e-51; ive 59; Mismatches 87; Indels (
                                                                                                                                                                                                                                       503 AA; 54079 MW; 33F3471EE21A0D32 CRC64;
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                       Pfam; PF00191; annexin; 4.
PRINTS; PR00196; ANNEXIN.
ProDom; PD000143; Annexin; 4.
01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDYKKALLLLSGEDD 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:| || : | :|
GDYRKILLKICGGND 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35,
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8K2N9;
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                  Similar to annexin All.
                                                                                                                                                                                                    SMART; SM00335; ANX; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similar to annexin A8
                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                 Local Similarity
nes 169; Conserv
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                  309
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                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                  Best Loca
Matches
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                                                                                                                                                                                                                                                                         82 GKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEYG
                                                                                                                                                                                                                                                                                                                                                                                       142 SSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELKWGTDEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 FITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALL
                                                                                                                                                                                                                                                      22 FDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSELT
                                                                                                                                                                                                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annexin; Calcium; Calcium-binding; Calcium/phospholipid-binding;
                                                                                                                                                                                                                     ä
                                                                                                                                                                                        DB 11; Length 327;
                                                                                                                                                                                                                       Indels
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC030407; AAH30407.1; -. MGD; MGI:1201374; Anxa8.
                                                                                                                                                       327 AA; 36724 MW; 56DB9CFAFA8C2B21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36787 MW; 2EB178E13738CF22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                    ; Score 840.5; DB 11;
; Pred. No. 2.9e-51;
49; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                               PRINTS; PRO0196; ANNEXIN.
ProDom; PDO000143; Annexin; 4.
SMART; SM00335; ANX; 4.
SEQUENCE 327 AA; 36724 MW;
                                                  InterPro; IPR001464; Annexin.
Pfam; PF00191; annexin; 4.
                                                                                                                                                                                      51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00223; ANNEXIN; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                    Query Match
Best Local Similarity 57.89
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00335; ANX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 LLSGED 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 NLVGTD 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9913;
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DB 6;

50.9%; Score 836.5;

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193 253 253 313 313

134

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TEKSELSGKFERLIVALMYPPYRYEAKELHDAMKGLGTKEGVIIEILASRTKNQLQEIMK 133
                                                                                                135 VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 SIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TVKGSPHFNPVPDAETLYKAMKGIGTNEQAIIDVLTRRSSAQRQQIAKSFKAQFGSDLTE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                               DLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ
                                                                                                                                                          194 WGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRS
                                                                                                                                                                                                                254 IPAYLAETLYYAMKGAGTDDHTLIRVWVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSG
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the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420.563-573 (2002).
BEMBL: AK090055; BAC41070.];
SEQUENCE 323 AA; 36356 WW; 9F69F57BCFAC6A85 CRC64;
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Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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49.2%; Pred. No. 2.4e-48;
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Best Local Similarity 49.28
Matches 155; Conservative
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Cheng W., Tsao F.H.C.;
Submitted (UUL-1997) to the EMBL/GenBank/DDBJ databases.
Cheng W., Tsao F.H.C.;
Submitted (UUL-1997) to the EMBL/GenBank/DDBJ databases.
Cheng W., Tsao F.H.C.;
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INDIRECT INHIBITOR OF THE THROMBOPLASTIN-SPECIFIC COMPLEX, WHICH
CHOUVED IN THE BLOOD COAGULATION CASCADE (BY SIMILARITY)
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                                                                                                                                                                   VYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAG-IDEAQVEQDAQALFQAGELK 193
                                                                                                            DLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQ 134
                                                                    15 TVTDFPGFDERADAETLRKAMKGLGTDEESILTILITSRSNAQRQEISAAFKTLFGRDLLD 74
                                                    TVTDFPGFDERADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLD 74
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
NCBI_TaxID=9986;
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55.9%; Pred. No. 5,4e-50;
ive 48; Mismatches 89;
            Pred. No. 5.6e-51;
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72 68 132 128 192

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Search completed: August 22, 2003, 21:35:26 Job time : 32.6667 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 15:48:20; Search time 1675.67 Seconds (without alignments)
14228.779 Million cell updates/sec

Perfect score: 981
Scoring table: US-09-970-969-5
Sequence: 1 atggcatgtggctgggtca......tgctctccggagaagatgac 981
Scoring table: IDENTITY_NUC
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Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784
Minimum DB seq length: 0
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e: EST:* 1: em_estba:* 2: em_estbum:* 3: em_estin:* 4: em_estin:*	6: em_estpl:* 7: em_estro:* 8: em_btc:* 9: gb_estl:* 10: gb_est2:* 11: gb_btc:* 12: gb_est4:* 13: gb_est4:* 14: gb_est5:* 15: em_estfun:* 16: em_estfun:* 17: em_gss_hum:* 18: em_gss_hum:* 19: em_gss_pln:* 20: em_gss_pln:*	21: em_gss_nam: 23: em_gss_mam: 24: em_gss_mus: 25: em_gss_pro:* 26: em_gss_phg:* 27: em_gss_phg:* 27: em_gss_phg:* 29: gb_gss1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	BC032093 Homo sapi	BM464122 AGENCOURT	BX441583 BX441583	BX379189 BX379189
SUMMARIES			No. Score Match Length DB ID	BC032093	BM464122	BX441583	BX379189
			80	=	12	13	13
			core Match Length DB ID	1602			
	æ	Query	Match	97.6			
			Score	957.8	874.4	868.2	828.4
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1076 bp mRNA linear EST 05-FEB-2002
ACENCOORT_6445585 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5540173
5', mRNA sequence.
BM464122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 2 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparetion: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12235 row: n column: 14
High quality sequence stop: 708.
Location/Qualifiers
rce
                                    814 AATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGT
                                                                                                                                                                                                                                      921 TAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCTCCGGAGAAGATGA
                                                                                                      GGGAGCTGGGACAGATGATCATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGA
                                                                                                                                                                        TCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoi
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases I to 1076)
NIH-MGC http://mgc.ncl.nlh.gov/.
National inatitutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Homo sapiens"
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/lab_host-"DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 874.4; DB 12;
Pred. No. 1.4e-223;
0; Mismatches 25;
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229 c
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Best Local Similarity 96.9%;
Matches 932; Conservative
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AUTHORS
TITLE
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COMMENT
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BM464122
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                               Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 26 Row: f Column: 11 This clone has the following problem: no 5' EST match. Location/Qualifiers
                                  Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATTGTGGCTCTGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      694 TCAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                   melanoma."
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly,
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart.
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                      DB 11;
                                                                                                                                                                                                /organism="Homo saplens"
/mol_type="make"
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/clone="iMaGE:3924873"
/tissue_type="Skin, melanotic me
/clone_lib="NIH_MGC_72"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                  97.6%; Score 957.8; DB 11
99.8%; Pred. No. 6.9e-246;
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337 c 364 g 452 t
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959; Conservative
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/clone_lib="Homo sapiens FETAL BRAIN"
/rolone_lib="Borain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

229 c 274 g 272 t 5 others
                                    Euteleostomi;
                                                                                                                Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
http://www.genoscope.cns.fr/
cgi-bin/Cluster.cgirseq-CSODF019AF066P1&cluster-2353.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF013AF066P1.
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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                                              Mammalia; Eutheria; Primates; Catarrhini; Hor
1 (bases I to 1071)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Pred. No. 6.4e-222;
L; Mismatches 5;
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/mol_type="mrna" db_xref="taxon:9606"
/clone="CSODFO19YK11"
/tissuc_type="feral" BRAIN"
/dev_stage="feral"
                                                                                                                                                                                                                                                                              sapiens"
                                                                                                                                                                                                                                                                           /organism="Homo
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al Similarity 99.3%;
870; Conservative
           sapiens (human)
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                                                                    ATTGTGGCTCTGAAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG
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BX398791 996 bp mRNA linear EST 13-MAY-2003 BX398791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA COLONE CSODI064YH19 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmall: seqrefégenoscope.cns.fr.web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-cS0D1064CD10QP16cluster-2353.r. Contact:
Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1064CD10QP1.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
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                                                                                                                                                                                                                                                                                                                                                                                    CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGATT
                                                                                                                                   CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA
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/db_xref="taxon:9606"
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/dol_type="mRNA"
/dol_type="mRNA"
/dol_type="mRNA"
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/clone="CSODEO09Y116"
/clone="Lb="dono saplens PLACENTA"
/clone="Lb="dono saplens PLACENTA"
/note="Vector: pCWSPORT_6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
Library was not normalized. 39 others
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                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

BM 11: Sequendscope.cns.fr, whe : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 2353.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cg1-bin/cluster.cg1?seq-CSODE009BE08QPl&cluster-2353.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODE009BE08QPl.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGCACAGGTTCTCAGAGGCACTGTGACTTCCCTGGATTTGATGAGCGGGCTGAT
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Pred. No. 2.1e-218;
....atrhes 30; Indels
                                                                                                                                                     1 (bases 1 to 1201)
11,W B., Gruber,C., Jessee,J. and Polayes,D.
11,W B., Gruber,C., Jessee,J. and normalization
Unpublished
Contact: Genoscope
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                                   BX417429.1 GI:30654405
5-PRIME, mRNA sequence.
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95.0%;
                                                                           sapiens (human)
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893; Conservative
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Homo sapiens (human)
Homo sapiens
           Homo
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primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the DONYSPORT 6 vector. Library was normalized. I 192 c 248 g 256 t 18 others
                                                                                                                                                                              GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT
                                                                                                                       GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCTGGACT
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                                                                                                                                               CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG
                                                                                                                                                                                                              ATTGTGGCTCTGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG
                                                                                                                                                                                                                                                              AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA
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                                                                Gaps
                                                 Length
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Pred. No. 1.8e-217;
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97.6%;
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RESULT 7 BX396240

//crganism="Homo saplens"
/mol_type="mRNA"
/do_xref="taxon:9606"
/do.xref="taxon:9606"
/clone="CSD1014Y109"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone=lab="Homo saplens placement of 25-NORMALIZED"
/clone="lab="Homo saplens placement of 25-NORMALIZED"
/clone= Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqreféqenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi/seq-Cs0bl014AE05Qpl&cluster=2353.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0bl014AE05Qpl.

I. 2062Linn/Qualifiers p mRNA linear EST 13-MAY-2003 COT 25-NORMALIZED Homo sapiens cDNA ö 267 141 327 201 387 261 447 507 567 441 ATTGTGGCTCTGATGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG 321 AAGGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA 381 627 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li (bases I to 1062)
Li W. B., Gruber, C., Jassee, J. and Polayes, D. Full-length, CDNA libraries and normalization 81 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 22 ATGGCACAGGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGCGGGCTGAT AAGGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA Gaps ch 86.5%; Score 848.2; DB 13; Length 1062; Il Similarity 99.4%; Pred. No. 1.5e-216; 850; Conservative 1; Mismatches 4; Indels 0; clone CSODI014YI09 5-PRIME, mRNA sequence. BX396240 1062 bp sapiens PLACENTA BX396240.1 GI:30624830

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others
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les 25;
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1201 bp mRNA linear EST 08-MAY-2003
BX379218 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI031Yal6 5-PRIME, mRNA sequence.
BX379218.1 GI:30452736
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/mol_cype="mans.saptcms"
/db_xref="taxon:9506"
/db_xref="taxon:9506"
/done="150010317A16"
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/clone_lib="Homo sapiens PlaCENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                            561
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr.
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODI031BA08QP1scluster-2353.r. Contact
Feng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI031BA08QP1.
                  CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA
                                                                                                                                      CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA
                                                                                                                                                                                              682 ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTTGCTGTT
                                                                                                                                                                                                                                                                     868 ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT
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 GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTGTTCTCCTTCAGGCTAAC
                                                            AGAGACCCTGATGCTGGAATTGATGAAGCTCCAAGTTGAACAAGATGCTCAGGCTTTATTT
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Li.W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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|1048 CTGTATWACATCAGG 1062
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Contact: Genoscope
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PERTINITION MASSAGES CONTROLLED BY THE PROPERTY OF THE PROPERT		BX358605   BY ANTERACGARACTTCTGGCAATTTAGAGCAACTACTCCTTGCTG   The control of the	clone CSODIO41YIÛ2 5-PRIME, mRNA sequence. BX358605 BX358605.1 GI:30382268 EST. Homo sapiens (human) Homo sapiens (human) Extracta: Craniata: Vertebrata: Euteleost.	Manmalla: Eutheria; Primates; Catarfili; Hominidae; Homo.  1 (bases 1 to 1076)  11 (bases 1 to 1076)  12 (bases 1 to 1076)  13 (bases 1 to 1076)  14 (bases 1 to 1076)  15 (bull-length cDNA libraries and normalization  Unpublished  Contact: Genoscope  Genoscope - Centre National de Sequencage  BP 191 91006 EVRY cedex - France  BP 191 91006 EVRY cedex - France  Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr  Library was constructed by Life Technologies, a division of	Invitrogen. This sequence belongs to sequence cluster 2353.r For more information about this cluster, see http://www.genoscope.cns.fr cluster, see http://www.genoscope.cns.fr cgd-bin/cluster.cg7seq-CSODIO41BED1QP1&cluster=2353.r. Contact : Feng Liang Email : filang @lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen com/ Invitrogen.com/ Invitrogen.com/ Invitrogen.com/ Invitrogen.com/ Invitrogen.com/ Invitrogen.com/ Invitrogen.com/ Composition 1600 Faraday Avenue Genoscope sequence ID : CSODIO41BED10P1. Location/Qualiflers 11076 //organism="Homo sapiens" //mol_type="mRNA" //dof_txscf="faxon:9606" //clone="CSODIO41Y102" //tissue_type="PLACENTA COT 25-NORMALIZED" //clone="Lib" Homo sapiens PLACENTA COT 25-NORMALIZED" //note="lst strand cDNA was primed with a NotI-oligo(dT)
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	AL542496 AL542496 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE012Y11 5-PRIME, mRNA sequence. 5-PRIME, mRNA sequence. AL542496. AL542496.2 GI:30547699 EST. Homo sapiens (human) Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1201) 1 (M.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished On Feb 15, 2001 this sequence version replaced gi:12874598. Genoscope	First 19100 EARI Cedex. France Email: seqref@genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2353.r For more information about this Cluster, see there.information about this Cluster, see there.information about this Cluster.  http://www.genoscope.cns.fr/ cgi-bin/cluster.gdi?seq=CSODE012BE07Qplccluster=2353.r. Contact Feng Liang Email: fliangellifetech.com URL: Location/Qualifiers 1.1201  /organism="Homo sapiens" //mol_type="mRNA" //mol_type="mRNA" //clone="CSODE012RI14" //clone="CSODE012RI14" //clone="Libraxon:9666" //clone="Libraxon:9666" //clone="Libraxon:9666" //clone="Libraxon:9666" //clone="Libraxon:9666" //clone="Libraxon:9666" //clone="Libraxon:9666" //clone="Taxon:9666" //clone="Taxon:9	Ilbrary was not normalized."  1 310 a 243 c 293 g 307 t 48 others  atch  2	22 ATGGCACAGGTTCTCAGAGGCACTGACTTCCTGGATTTGATGAGGGGGCTGAT 81 167 ATGGCACAGGTTCTCAGAGGCACTGACTTCCTGGATTTGATGAGGGGGCTGAT 81 167 ATGGCACAGGTTCTCAGAGGCACTGACTTCCTGGATTTGATGAGGGGCTGAT 22 82 GCAGAAACTCTTCGGAAGGCATGAAAGGCTTGGGCACAGATGAGAGAGCATCCTGACT 14 227 GCAGAAACTCTTCGGAAGGTATGAAAGGCTTGGGCACAGATGAGAGAGCATCCTGACT 28 142 CTGTTGACATCCTCGGAAGTAATGAAGGCTTGGGAAATCTCTGCAGCTTTTAAGACTCTG	

ched, double-strand cDNA word into the Not I and Eco	233 c 274 g 278 t 4 others	85.2%; Score 835.8; DB 13; Length 1076; Similarity 97.4%; Pred. No. 3.3e-213; 6; Conservative 4; Mismatches 16; Indels 3; Gaps 2;	GGCACAGGTTCTCAGAGGCACTGTGACTGCACTTCCCTGGATTTGATGAC	cecercar 25	GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGAGCATCCTGACT 141 	STTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 20	CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAATCTCTGCAGCTTTTAAGACTCTG 370	TTTGGCAGGGATCTTCTGGATGACCTGAAATCAGAACTAACT			AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA 381	AAGGGAGCTGGAACAAATGAAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA 550	GAACTGAGAGCCATCAAAAGTTTATGAAGAAGAATATGGCTCAAGCCTGGAAGATGAC 441 	2		26		CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAGTTTATCACCATCTTTGGAACA 621 	CGAAGTGTGTCTCATTTGAGAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 681	GAAGTGT-TCTCATTTGAGAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 849	ATTGAGGAAACCATTGACGGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT 741	ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT 909	GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGCCCTCTATTATGCTATGAG 801		61	GGAGCTGGGACAGATGATCATACCCTCATCAGAGTYATGGTTTCCAGGAGTGAGATTGAT 1029	CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTTT 910	CIGITIA CATCAGGAGAGITIAGGAGRATITKCCACICITITWIT 1076
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RESULT 11 BX402751

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Contact: Genoscope

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY Cedex - France

BP 191 91006 EVRY Cedex - France

Email: seqref@enoscope.cns.fr, Web: www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

2353.r For more information about this cluster. see

http://www.genoscope.cns.fr/

cgi-bh/cluster.cgi/seq-CS1A1021ZG030P1&cluster=2353.r. Contact:

Feng Liang Email: iflianglifetech.com URL:

http://fulllength.invitrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CSIAI021ZG03QP1.

Location/Qualifiers

location/Qualifiers

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//clone_lib="Homos sapiens PLACENTA COT 25-NORMALIZED"
//note="lst strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWYSPORT 6 vector. Library was normalized."
216 c 257 g 256 t 1 others
BX402751 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO84YA05 5-PRIME, mRNA sequence.
BX402751 GI:30607254
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                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1007)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Ouery Match 84.8%; Score 831.6; DB 9; Length 1201; Best Local Similarity 95.0%; Pred. No. 4.6e-212; Matches 911; Conservative 11; Mismatches 26; Indels 11; Gaps 6;	Oy 22 AIGGCACAGAGTTCTCAGAGGCACTGTGACTGACTTCCCTGGATTTGATGAGGGGGCTGAT 81	Qy         82 GCAGAAACTCTTCGGAAGGCTATGAAAGGCTTGGGCACAGATGAGGAGGCATCCTGACT         141	OY 142 CTGTTGACATCCCGAAGTAATGCTCAGCGCCAGGAAATCTCTGCAGCTTTTAAGACTCTG 201 11111111111111111111111111111111111	QY 202 TTTGGCAGGGATCTTCTGGATGCCTGAAATCAGAAACTTGAAAAATTA 261	Oy 262 ATTGTGGCTCTGAAACCCTCTCGGCTTTATGATGCTTATGAACTGAAACATGCCTTG 321	OY 322 AAGGGAGCTGGAACAAATGAAAAGTACTGACAGAAATTATTGCTTCAAGGACACCTGAA 381	Qy         382 GAACTGAGAGCCATCAAACAAGTTTATGAAGAATATGGCTCAAGCCTGGAAGATGAC 441	Db   628   GTGGTGGGGACACTTCAGGGTACTACCAGGGATGTTGGTGGTTCTCCTTCAGGCTAAC   687     Qy   502   AGACACCTGATGGTGAATTGATGAGGTTGAAGATGAAGATGAAGTTGAAGATGAT	Qy 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA 621	Oy 622 CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTATATCAGGATTTCAA 681	Oy 682 ATTGAGGAAACCATTGACCGCGAGACTTTGGCAATTTAGAGCAACTACTCCTTGCTGTT 741  1111111111111111111111111111111111	Qy 742 GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGACCCTCTATTATGCTATGAAG B01	Qy 802 GGAGCTGGGACAGATGATCATACCTCATCAGAGTCATGGTTTCCAGGAGTGAGATTGAT 861	OY 862 CTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTATTCCATGATT 921	QY 922 AAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTCTGCTGCTCCTCCGGAGAAGATGA 980	RESULT 13 AL517516 LOCUS AL517516 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
Qy       44.2       GTGGTGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTGTTCTCCTTCAGGCTAAC       50.1         LILILILILILILILILILILILILILILILILILILI	Oy 502 AGAGACCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATT 561	OY 562 CAGGCTGGAGAACTTAAATGGGGGACAGATGAAGAAAAGTTTATCACCATCTTTGGAACA 621 	QY 622 CGAAGTGTGTCTCATTTGAGAAAGGTGTTTGACAAGTACATGACTTTATCAGGATTTCAA 681 	QY 682 ATTGAGGAAACCATTGACCGGGGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT'741	Oy 742 GTGAAATCTATTCGAAGTATACCTGCCTACCTTGCAGAGCCCTCTATTATGCTATGAAG 801 Db 891 GTGAAATCTATTCGAAGTATACCTGCCTACCTGCAGAGCCCTCTATTATGCTATGAAG 950	OY 802 GGAGCTGGGACAGATGATACCCTCATCAGAGTCATGGTTTCCAGGAGTGAGATT 858	RESULT 12 AL547761 LOCUS AL547761 DEFINITION AL547761 DEFINITION AL547761 Homo saptens PLACENTA COT SOUNALIZED Homo saptens CDNA COLONG CLONG CASHOLO TAILS CON CLONG CASHOLO TAILS CON CONTRACT TO TAIL SACRIFICATION ALSO TAILS CON CASHOLO TAILS CASHOLO TAILS CON CASHOLO TAILS CON CASHOLO TAILS		ELMETYOCEA, MetaZooa; CHORTGATA; VERTEDRATA; Buteleostomi; REFERENCE 1 (bases 1 to 1201) AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D. TTTLE Full-length Chia interies and normalization		Denotocyce  BP 191 91006 EVRY cedex. France  Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  Library was constructed by Life Technologies, a division of  Touttroan This sequescope belong to suppose a particular of	Conta	http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODIO17CE060P1. FEATURES. Location/Qualifiers		COT 25-NORMALIZED"  S PLACENTA COT 25-NORMAL:  RAS primed with a Noti-olariched, double-strand	da Ta

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AL541412 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE006Kyllo AL54H12 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE006Kyllo AL54H1E, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Fill-length cDNA libraries and normalization
Unpublished
On Feb 15, 2001 this sequence version replaced gi:12872460.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Linvitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODE006DE05QPl&cluster=2353.r. Contact :
Ggi-bin/cluster.gi?seq-CSODE006DE05QPl&cluster=2353.r. Contact :
http://tulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODE006DE05QPl.
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                                                                          502 AGAGACCCTGATGCTGGAATTGATGAAGCTCAAGTTGAACAAGATGCTCAGGCTTTATTT
                                                                                           861 TCTGTTTAACATCAGGAAGGAGTTTAGGAAGAATTTTGCCACCTCTCTTTATTCCATGAT
   442 GTGGTGGGGGACACTTCAGGGTACTACCAGCGGATGTTGGTGGTTCTCCTTCAGGCTAAC
                      ATTGAGGAAACCATTGACCGCGAGACTTCTGGCAATTTAGAGCAACTACTCCTTGCTGTT
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/tissue_type="PLACENTA"
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Library was not normalized." 27 others
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cgi-bin/cluster.cgi?seq=CSODA003CC03QPl&cluster=2353.r. Contact :
Feng Liang Email : fliangelifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODA003CC03QPl.
Location/Qualifiers
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 (bases 1 to 1201) Li.M.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2353.r For
more information about this cluster, see
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84.5%; Score 828.6; DB 9; Length 1201;
Best Local Similarity 93.5%; Pred. No. 3e-211;
Matches 880; Conservative 14; Mismatches 40; Indels 7;
CSODA003YF05 5-PRIME, mRNA seguence.
                                  AL517516.2 GI:30534896
                                                                        Homo sapiens (human)
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Contact: Genoscope
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/clone_lib="Homo sapiens PLACENTA"

/clone_lib="Homo sapiens PLACENTA"

/note="Vector: pCMVSPORT_6" ist strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

Library was not normalized."

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                                                                            Score 822; DB 9;
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Contact: Genoscope General de Sequencage
BP 191 91006 EVR cedex - France
BP 191 9100 BP 191 FILE FECH CONTACT - Sequence Cluster 2353.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cg1-bin/cluster.cg1?seq=CSODE004CB11QP1&cluster=2353.r. Contact : Feng Liang Bpa11 : filangelifetech.com URL :
FRANCE FRANCE Genoscope sequence ID : CSODE004CB110P1.
FRANCE FRANCE Genoscope sequence ID : CSODE004CB110P1.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="taxon:9606"
/clone="type="PLACENTA"
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/clone="type="pcMVSpORT_6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORY sites of the pcMVSpORT 6 vector.
Library was not normalized."
Library was not normalized."
5 others
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On Feb 16, 2001 this sequence version replaced
Contact: Genoscope
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
 ATTAAGGGAGATACATCTGGGGACTATAAGAAAGCTCTTC
                       Score 820.4; DB 9;
Pred. No. 4.3e-209;
5; Mismatches 1;
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llarity 99.1%;
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